WO 01/57274 PCT/US01/00666

Expression of Genes in Human Heart

Table 4 (413 pages) presents expression, homology, and
functional information for the genome-derived single exon
probes that are expressed significantly in human heart.

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Table 4
Single Exon Probes Expressed in Heart

יויייייייייייייייייייייייייייייייייייי	Top Hit Descriptor																Annual Control of the					ξ.													
201 1100	Top Hit Database Source																																		
5	Top Hit Acession No.																		,																
	Most Similar (Top) Hit BLAST E Value															,																			
	Expression Signal	4.41	17.08	2.14	7.97	1.87	4.97	1.01	0.95	7.45	86.0	3.03	2.62	2.34	3.7	1.52	8.97	0.87	0.99	1.71	. 5.94	0.89	0.89	1.03	1.76	0.78	5.08	2.07	1.92	1.92	9	5.89	4.9	2.9	1.6
	ORF SEQ ID NO:		20647								21620														24402										25678
	Exon SEQ ID NO:	10386	10797	10947			11523	11596			11744	11830	12008	ı	13074			13429	13521	14002	14064		14084	14141			14851		15140	15140	15248				19451
	Probe SEQ ID NO:	442	871	1029	1280	1597	1619	1694	1715	1721	1848	1935	2119	2233	3149	3403	3471	3513	3607	4102	4164	4184	4184	4242	4730	4779	4976	4988	5217	5217	5328	5436	5483	2509	2668

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Table 4
Single Exon Probes Expressed in Heart

ongie cyon Piopes Cypresseu III near	Top Hit Descriptor																		Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18	Haemophilus influenzae Rd section 31 of 163 of the complete genome	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds	Mus musculus AT3 gene for antithrombin, complete cds	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product	601651038R1 NIH_MGC_81 Hamo sapiens cDNA clone IMAGE:39345923'
jie Exori Probe	Top Hit Database Source																		TN	NT I	N TN	NT FE	NT	_ LN		SWISSPROT	IN TN	d IN	T HUMAN
) Jic	Top Hit Acession No.																		9.9E+00 AJ239028.1	9.8E+00 U32716.1	9.6E+00 AF242432.1	9.6E+00 AF242432.1	L11433.1	9.4E+00 L11433.1	AB043785.1	9.3E+00 P11210	9.1E+00 AF095609.1	9.1E+00 AF095609.1	8.9E+00 BE971806.1
	Most Similar (Top) Hit BLAST E Value																		9.9E+00	9.8E+00	9.6E+00	9.6E+00	9.4E+00	9.4E+00	9.4E+00	9.3E+00	9.1臣+00	9.1E+00	8.9E+00
	Expression Signal	1.41	1.84	1.61	1.61	1.29	1.3	3.58	1.26	3.7	2.31	2.84	2.91	1.73	1.73	2.19	1.62	2.11	13.31	1.54	1.32	1.32	2.72	2.72	5.91	2.97	2.07	2.07	5.51
	ORF SEQ ID NO:	25700		26404	26405	26769	27012	27569	27758		28355	•	28840	28150	28151			25230	25701	26745	28046	28047	22389	22390	22612	27271	24932	24933	25687
	Exon SEQ ID NO:	15599	15769	16244	16244	16577	16820	17364	17534	17961	19472	18266	18555	17906	17906	18606	19094	19280	15600	16549	17805	17805	12499	12499	12820		15163	15163	1 1
	Probe SEQ ID NO:	2690	5863	6382	6382	2699	6942	7494	7684	8070	8219	8390	8666	8757	8757	8792	9464	9760	5691	6999	7955	7955	2631	2631	2893	7206	5239	5239	5678

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	ı				"		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5848	15754		1.71	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
5848	15754	25872	1.71	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
433	10378		1.75	8.4E+00	5031804 NT	TN	Homo saplens insulin receptor substrate 1 (IRS1) mRNA
7439	16452	26642	3.68	.8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
8209	18381		2.31	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
6346			2.07	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8989	16747	26940	1.53	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8989	16747	79697	1.53	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5544	15460	25531	2.58	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5'
7085	16962	27155	3.83	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
7085	16962	27156	3.83	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2947	12874	22671	4.2	7.2E+00	L12051.1	TN	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
2947	Į.	22672	4.2	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
6239	16105	26254	1.3	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
6239	16105	26255	1.3	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7535	17386		8.48	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
8690	18577	28860	3.26	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
7735	17585	27809	2.98	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
8575	18443	28712	1.85	7.0E+00	022469	SWISSPROT	WD-40 REPEAT PROTEIN MSI3
6818	16697	26889	2.72	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
7925	17775	28015	1.3	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
6614	16494	26680	1,45	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291860 5'
6614	16494	26681	1.45	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291860 5'
7707			27.6	OUT JO 8	208900	TOddoo!/Wo	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: LOI ITER CAPSID PROTEINS VP5 AND VP81
70607	47740	07057	1000	001100		TOGGGGWG	HVPOTHETICAL 157 0 KDA PROTEIN C38C40 5 IN CHROMOSOME III
2007			20.0	0.00		TO GOOMS	HIPTON ATE CHARGE (HEV) THE MONOBHOSE HARSE (HASE)
7796	_L		2.1	6.6E+00	Q9ZE07	SWISSPROI	UNIDITALE RINASE (UN) (UNIDINE MONOFIDOSFIDALE RINASE) (UNIT RINASE)
7796		27882	2.1	6.6E+00	Q92E07	SWISSPROI	URIDITATE NIVASE (UN) (URIDINE MUNOFIDOSTITATE NIVASE)
8471	1		2.17	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C
7296	17172	27372	8.32	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52, COAT PROTEIN GP36]
7616	17467	27686	1.44	6.2E+00	AY010901.1	NT	Schizophyllum commune unknown mRNA
5928	15833	25956	7.16		AF155142.1	NT	Mus musculus mixed lineage kinase 3 (MIk3) and two pore domain K+ channel subunit (Konk6) genes, complete cds
3479	1	Ĺ	0.84	5.8E+00		Z	Homo sapiens DESC1 protein (DESC1), mRNA
2			1,3,3	12.722			

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יישור בארון	Top Hit Descriptor	LYCOPENE BETA CYCLASE	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 67	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C;	LIPOVITELLIN LV-2]	RHODOPSIN	RHODOPSIN	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)	PROBABLE, ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162	Eunice australis histone H3 (H3) gene, partial cds	PM0-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5	Homo sapiens chromosome 21 segment HS21C080	Methanococcus Jannaschii section 111 of 150 of the complete genome	Archaeoglobus fulgidus section 63 of 172 of the complete genome	602072585F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'	602072585F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'	Murine I gene for MHC class II(Ia) associated invariant chain	Plasmodium falciparum R29R+var1 gene, exon 1	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	genes, complete cds	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)	wf67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692.3'	YY1 PROTEIN PRECURSOR	GENE 68 PROTEIN	GENE 68 PROTEIN
	Top Hit Database Source		SWISSPROT	¥.			. 1	ISSPROT	NT	SWISSPROT		SWISSPROT) LN	NT TN	F E	EST_HUMAN F	HUMAN	T_HUMAN	I I		NT TN	EST_HUMAN 6	EST_HUMAN 6	V IN			5 5	SWISSPROT (EST_HUMAN V		\Box	SWISSPROT
	Top Hit Acession	00 Q55276	00 P11990	4L161571.2		00 Q91062	00 Q17094	Q17094	_43126.1	00 P54098	00 Q27905	00 P09182	AF162445.2	Z83860.1	AF185255.1	00 AW750067.1	BF240552.1	BF240552.1	AL163280.2	U67569.1	30 AE001044.1	00 BF530893.1	10 BF530893.1	X13414.1	Y13402.1		AF240786.1	00 P16444	00 P13983	213983	00 AI809013.1	00 023810	00 P28964	00 P28964
	Most Similar (Top) Hit BLAST E Value	5.6E+00	5.5E+00	5.5E+00] 	5.4E+00	5.4斤+(5.4E+00	5.3E+00	5.3E+00	5.3E+00	5.1E+00	5.0E+(5.0E+00	4.8E+00	4.8E+00	4.7E+00	4.7E+00	4.7E+00	4.6E+00	4.5E+00	4.4E+00	4.4E+00	4.4E+00	4.3E+00	1	4.3E+00	4.2E+00	4.2E+(4.2E+00	4.2E+00	4.1E+00	4.1E+00	4.1E+
	Expression Signal	2.44	2.65	1.94		1.62	1.44	1.44	1.54	4.04	3.21	1.21	3.06	10.53	9.43	5.01	2.03	1.92	4.01	1.48	1.99	96.0	96.0	1.55	2.01		7.49	2.92	1.57	1.57	5.45	7.65	3.31	3.31
	ORF SEQ ID NO:	28166	28165				27849	27850	24354		29003	27730	28050	28749			20071	20071	22958	26617	28986	22723	22724		26420		28368		26186	26187	27249	26553	26618	26619
	Exon SEQ ID NO:	17919	17918	18773	l				14561	16590		17505	17809	18477	13879	16847		10251			18693	12931	12931	15671	16259	ı	18116	15306	16043		17059	16376		
	Probe SEQ ID NO:	8770	8769	8967		6593	7769	7769	4675	6710	8839	7655	7959	8610	3972	6970	286	287	3236	9259	8881	3003	3003	5764	6398		8235	5387	0909	0909	7182	6517	6577	6577

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Single Exon Probes Expressed in Heart

	_	_	_	_		_	_	_					_				_						_					
. Top Hit Descriptor	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus	602247938F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5	HYPOTHETICAL PROTEIN HVLF1	601507510F1 NIH_MGC_71 Hamo sapiens cDNA clone IMAGE:3909051 5'	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IBP-1) (IGF-	BINDING PROTEIN 1)	CELL DIVISION PROTEIN FTSY HOMOLOG	CYTOCHROME C OXIDASE POLYPEPTIDE III	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN	(ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRÚCTURAL PROTEINS NS7 NS2A NS2A NS4A AND NS4B: HEI IGASE (ANS4): BNA-DIRECTED BNA POLYMEDASE (ANS5)	N. tabacum chitinase gene 50 for class I chitinase C	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2	X.laevis mRNA for M4 muscarinic receptor	Homo sapiens NF2 gene	nr18a12.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMACE:1168318 similar to gb:A10416 METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN);	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE;4277748 5	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
Top Hit Database Source	LN	EST_HUMAN	SWISSPROT	EST_HUMAN		SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	į	TORGERME	NT	Ā	EST_HUMAN	EST_HUMAN	SWISSPROT	NT	NT	NT	EST HUMAN	F	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT
Top Hit Acession No.	4.1E+00 U57503.1	4,1E+00 BF692425.1	P09716	4.1E+00 BE885880.1	٠,	P47876	033010	P14546	P07564		D07564	X64518.1	3.9E+00 AF055466.1	3.9E+00 BE814357.1	3.9E+00 BE814357.1	P39299	3.9E+00 M23907.1	X65865.1	Y18000.1	3.9E+00 AA661489.1	3.8E+00 AE001562.1		3.7E+00 AL161539.2	3.7E+00 BF669279.1	3.7E+00 BF669279.1	3.6E+00 AV761055.1	3.6E+00 AE004447.1	3.6E+00 AE004447.1
Most Similar (Top) Hit BLAST E Value	4.1E+00	4,1E+00	4.1E+00 P09716	4.1E+00		4.1E+00 P47876	4.0E+00 O33010	4.0E+00	4.0E+00 P07564		4 0E+00 P07564	3.9E+00 X	3.9E+00	3.9E+00	3.9E+00	3.9E+00	3.9E+00	3.9E+00 X65865.1	3.9E+00 Y18000.1	3.9E+00	3.8E+00	3.8E+00	3.7E+00	3.7E+00	3.7E+00	3.6E+00	3.6E+00	3.6E+00
Expression Signal	2.95	2.31	2.89	12.46		1.86	1.37	2.17	3.34	i.	78 8	3.89	0.99	2.47	2.47	4.46	4.68	2:32	3.09	5.58	2.4	1.18	10.09	2.13	2.13	2.1	3.66	3.66
ORF SEQ ID NO:	26684					25241	26285	28164	28934		28035			25454	25455				28120	28816		26982		28872				27091
Exon SEQ ID NO:	16497		18139	18216		- 1	ı	17917	18648		18648	13375	14124	15391	15391	16002	16218	16719	17879	18532	12459	16789	13845	18586	18586	10516	16899	16899
Probe SEQ ID NO:	6617	7576	8229	8339		9672	9290	8768	8835		8835	3459	4226	5471	5471	6108	6355	6840	8695	8715	2588	6911	3936	8730	08/30	8/9	7022	7022

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Single Exon Probes Expressed in Heart

Probe SEQ ID 8 NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8228	18110		92 6	3 RF+00	3 RE+00 MGR795 1	·	Escherichia coli glycerophosphate dehydrogenase (glpD) gene, partial cds, and the translation start site has been verified (glpC), and repressor protein (glpR) genes, complete cds.
3209	13133	22934	1.04	3.5E+00		NT.	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
1496	11400	21260	3.57	3.4E+00		LN L	Brassica napus RPB6d mRNA, complete cds
2532	12406	22298	1.02	3.4E+00		NT	Homo sapiens chromosome 21 segment HS21C078
6354	16217		2.41	3.4E+00 P04052	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7889	17739		3.17	3.4E+00	7.1	TN	Saccharomyces cerevisiae MSS1 gene, complete cds
3818	18631	28919	1.92	3.4E+00	3.4E+00 L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
5036	14908	24679	1.41	3.3E+00	7662155 NT	N	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA
5036	14908	24680	1.41	3.3E+00	7662155 NT	TN	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA
492	10435		1.39	3.2E+00		TN	D.rerio zp-50 POU gene
3938	10435		62.0	· 3.2E+00	X96422.1	NT	D.rerio zp-50 POU gene
9439	15359		2.66	3.2E+00	3.2E+00 P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5439	15359	25416		3.2E+00 P12783	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5808	15713	25825	2.06	3.2E+00 P18931	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
808	15713	25826	2.06	3.2E+00 P18931	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6569	16427	50997		3.2E+00	3.2E+00 Y13655.1	NT	Chlamydomonas reinhardili chloroplast DNA for rps9, ycf4, ycf9, rps18 genes
6269	16427	26610	2.35	3.2E+00		NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7221	17098		6.33	3.2E+00	3.2E+00 P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
491	17361	27567	1.17	3.2E+00		TN	S.cerevisiae threonine deaminase (ILV1) gene, complete cds
7837	17687	27932	1.69	3.2E+00	3.2E+00 AB016081.2	LN	Oryzias latipes OIGC6 gene for guanylyl cyclase C, complete cds
6806	18863		4.32	3.2E+00		IN	Sus scrofa choline acetyltransferase gene, promoter region
2282	15497	25574	2.42	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
000/	16877	27067	4.35	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
7000	16877	27068	4.35	3.1E+00 P49894	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
7334	17238		3.8	3.1E+00 Q14957	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
7920	17770	28009	4	3.1E+00 P49365	P49365	SWISSPROT	DEOXYHYPUSINE SYNTHASE (DHS)
	,		C	L		1000	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN B); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NOON NICES AND NICES A
8/2g	1/908		3.78	3.1=+00/F33515	F33515	SWISSPRO	NOZA, NOZB, NOS#A AND NOS#B, THELICAGE (NOS), KINA-DIKECTED KNA POLTMERAGE (NOS)]
8774	18591		3.35	3.1E+00	3.1E+00 S56660.1	μ	retinoic acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]

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Table 4
Single Exon Probes Expressed in Heart

Probe	Exon Ci Ci Ci		Expression	Most Similar (Top) Hit	Top Hit Acession	Top Hit	Top Hit Tow Hit Tow Hit Descriptor
NO:			Signal	BLAST E Value	o Z	Source	I OP THE Descriptor
2807	12737		1.06	3.0E+00	8923984 NT	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
5273	15195		1.63	3.0E+00	3.0E+00 X53096.1	LN	Saureus genes encoding Sau96i DNA methyltransferase and Sau96i restriction endonuclease
6245	16111	L	9.5	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7164	17041		1.45	3.0E+00	3.0E+00 X67838.1	TN	B.napus DNA for myrosinase
0021	, 0 0	000	ŭ	00.000		TOGGSSIMS	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE PIOCEE)
92/4	_	70007	0.0	3.05+00		SW ISSI NO	
							RETINAL GUANYLYL CYCLASE 2 PREGURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE
8374	18251	28202	6.51	3.0E+00 P51842	P51842	SWISSPROT	F) (GC-F)
1964	11858	21747	2.56	2.9E+00	2.9E+00 AE002225.2	INT	Chlamydophila pneumoniae AR39, section 53 of 94 of the complete genome
6129	15976		1.63	2.9E+00		NT	F.pringlei gdcsPA gene for P-protein of the glycine cleavage system
6282	16146	_	4.47	2.9E+00 014514	014514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6282	16146		4.47	2.9E+00 014514	014514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6410	16271	26433	5.19	2.9E+00 P46589	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
1441	11346	21212	67.3	2.8E+00	2.8E+00 AF186398.1	TN	Buxus harlandii maturase K (matk) gene, partial cds; chloroplast gene for chloroplast product
1615	11519		3.12	2.8E+00		NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
6325	16188		4.78	2.8E+00		TN	Mus musculus endomucin (LOC53423), mRNA
230	10199	20012	4.63	2.7E+00	LN 9086799	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
230	10199		4.63	2.7E+00	9026299	LN LN	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
5408	15327	25377	1.75	2.7E+00 L1	4005.1	NT.	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
7185	17062		2.21	2.7E+00	_116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7996	17846		2.16	2.7E+00		EST_HUMAN	CMO-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
4576	14467	24253	4.35	2.6E+00	2.6E+00 AF068749.1	TN	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5405	15324	25373	1.97	2.6E+00	LN 1095579	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5405	15324	25374	1.97	2.6E+00	6755601 NT	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
6533	16391		5.45	2.6E+00	2.6E+00 AF235502.1	LN.	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
9699	16576	26767	1.2	2.6E+00	2.6E+00 AJ132180.1	¥	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
9699			1.2	2.6E+00		Ę	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
7567	1	27634	2.95	1		N L	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7927	17777		1.52	2.6E+00	9055193 NT	F	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
9711	19649		2.31		11419220	TN	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1448	11353	21216	2.08	2.5E+00 A.	1271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1448	11353	21217	2.08	2.5E+00	AJ271844.1	TN	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
2225	15468		2.33		P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
2225	15468		2.33	2.5E+00		SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5886	15468	25537	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5886	15468		1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6561	16419		1.34	2.5E+00	AW949158.1	EST_HUMAN	QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA
7264	17141	27334	1.75	2.5E+00	D50307.1	ZI.	Rice DNA for aldolase C-1, complete cds
9086	18861		2.26	2.5E+00	AF289665.1	N	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
2980	12907	22707	0.86	2.4E+00	M24282.1	TN	Chicken alpha-3 collagen type VI mRNA, 3' end
4816	14699	24485	7.62	2.4E+00	4503352 NT	N L	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
5657	15569	25664	4.19	2.4E+00		SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
6733	16613	26802	2.14	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
6733	16613	26803	2.14	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
6780	16659		2.63	2.4E+00	AE001486.1	Г	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
7026	16903		1.71	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
7125	17002	27194	9.45	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN.B)
7771	17621	27853	2.5	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
7771		27854	2.5		P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
7820		27911	2.18	2.4E+00	X92511.1	NT	H:sapiens CTGF gene and promoter region
7881	17731		6.49	2.4E+00	P09099	SWISSPROT	XYLULOSE KINASE (XYLULOKINASE)
7914	17764	28002	1.67	2.4E+00	BE326702.1	EST_HUMAN	hr63f06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
7914			1.67	2.4E+00	BE326702.1	EST_HUMAN	hr63f06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
8428	18302	28558	1.77	2.4E+00	Y14079.1	Z	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPFKD operon and downstream
8565	18554	28839	2.52	2.4E+00	AF158652.2	LN.	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene. ApxSC-c allele, complete cds
1233	1_	1_	9.36	2.3E+00			G.domesticus artificial single chain antibody gene (L3)
4031	L		1.28	2.3E+00	AJ401081.1	LN	Bos taurus partial cytb gene for cytochrome b
6408		26431	2.22	2.3E+00	6978554	NT.	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
6479	19766		2.3		P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
6573	16431	26613	1.53	2.3E+00	X60265.1	NT.	M.mazei dnaK and dnaJ genes homologues coding for DnaK and DnaJ
7289	17165	27364	1.81	2.3E+00	011127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)
8888	18793		2.6	2.3E+00	BF541987.1		602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
8988	18793	29084	2.6	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'

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Table 4
Single Exon Probes Expressed in Heart

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Probe SEQ ID NO:	Exon SÉQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
9428	19584		4.01	1.8E+00	AF314254.1	IN	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
9204	19119		2.4	1.8E+00	9506404 NT	TN	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA
8966	19429		1.34	1.8E+00	BF316805.1	EST_HUMAN	601903309F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135586 5'
1092	11008	20849	1.92	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2225	12110		3.25	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2321	12202		1.02	1.7E+00		EST_HUMAN	oz43h05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4356	14252	24037	0.84	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5448	15369		1.48	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5448	15369		1.48	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5664	15575	25673	3.58	1.7E+00		SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)
7014	16891		1.29	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
7282	19467	27355	2.15	1.7E+00		SWISSPROT	HOMEOBOX PROTEIN DLX-3
7282	19467	27356	2.15	1.7E+00	060479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
8874	18686	28977	1.78	1.7E+00	W22424.1	EST_HUMAN	67B7 Human retina cDNA Tsp509l-cleaved sublibrary Homo sapiens cDNA not directional
							tu82d07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.t1
9384	19044	25306	1.37	1.7E+00	AI678443.1	EST_HUMAN	MSR1 repetitive element ;
							qf50b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.t1 L1
9860		25185	2.26	1.7E+00		EST_HUMAN	repetitive element ;
1989			16.73	1.6E+00		NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
1997	11891	21783	3.61	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2003	11896	21788	1.96	1.6E+00	Y11344.1	NT	Mus musculus ST6GallNAcIII gene, exon 2
2238	12122		1.48	1.6E+00	X98373.1	NT	B.napus gene encoding endo-polygalacturonase
Ö			i c	20.70		HOL	zd25f01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5 similar to
1987		90077	20.2	1.0E+00	W 36420.1	EST HUMAN	SULZBOUS INFACET TELFOLOSTIVITIES STRUTTASE (FLOWARY), SOJESPOSTA NIEL MOO AE Home somione and Alma INMACE JAAARDA 21
0840			7.0	1.00+00	Dr3/00/7.1	NEW TOTAL	
4255			1.44	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4255		23929	1.44	1.6E+00	7.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5016	14890	24657	3.14	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcili gene, exon 2
5016	14890	24658	3.14	1.6E+00		TN	Mus musculus ST6GalNAcili gene, exon 2
5558	15474		2.19	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end
6296	16160	26317	2.64	1.6E+00	BE697267.1	EST_HUMAN	RC0-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA

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G cd cd cd	Exon			Most Similar		Teo H	H ao L
SEQ ID NO:	0)	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLAST E Value	Top Hit Acession No.	Source	Top Hit Descriptor
6681	16561		1.21	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
6881	16760	26958	3.56	1.6E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
7444	19465	26646	1.3	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-l
7444	19465		1.3	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-l
7611	17462	27679	1.29	1.6E+00		EST HUMAN	ph6b6_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6b6_19/1TV
7852	17702	27946	1.25	1.6E+00		EST_HUMAN	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA
7852			1.25	1.6E+00	1	EST_HUMAN	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA
8217	15520	25601	5.86	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgasel) gene, promoter region
8944	18752	29047	3.25	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
9902	19379		1.65	1.6E+00	AV764043.1	EST_HUMAN	AV764043 MDS Homo sapiens cDNA clone MDSDAH08 5'
30	10017	19812	4.29	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (Jdp-2) mRNA, complete cds
231	10200	20014	1.76	1.5E+00	AE002201.2	NT	Chlamydophila pneumoniae AR39, section 32 of 94 of the complete genome
605	10541		1.79	1.5E+00	6752961 NT	Į.	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA
2359	12239	22135	2.46	1.5E+00	AJ131402.1	与	Potato virus A RNA complete genome, isolate U
2468	12344	22237	2.02	1.5E+00	6678350 NT	F	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tram1), mRNA
3099	12239	22135	2.22	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3329	13249	23054	0.82	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5856	15762	25880	2.71	1.5E+00	R17879.1	EST_HUMAN	yg10e02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5'
6230	16096		1.42	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
6250	16116		29.13	1.5E+00		SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
6250	16116	26269	29.13	1.5E+00		SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BATZ-DAL5 INTERGENIC REGION PRECURSOR
7671	17521	27747	7.56	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
7782	17632		1.71	1.5E+00		EST_HUMAN	602035771F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183865 5'
7856	17706	27951	1.96	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
7856	17706	27952	1.96	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares refina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
8702	18520	28802	3.91	1.5E+00	7.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547P243 3'
8828	18641		10.73	1.5E+00	X07380.1	NT	Maize mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene
9223	18946		1.5	1.5E+00	6753287	IN	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA
9596	19178		2.89	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
0696	19243		1.42	1.5E+00	6978492 NT	NT	Rattus norvegicus 5 - Lipoxygenase (Alox5), mRNA
27	10014	19808	1.28	1.4E+00	7661685 NT	Ŋ	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
27		19809	1.28	1.4E+00	7661685	뉟	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2231	12116		0.95	1.4E+00	AF053357.1	Z	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds

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Top Hit Descriptor	Ovis aries prion protein gene, complete cds	Human papillomavirus type 7 genomic DNA	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Chlamydia muridarum, section 55 of 85 of the complete genome	Chlamydia muridarum, section 55 of 85 of the complete genome	Homo sapiens Mad4 homolog (MAD4) mRNA	CM0-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA	CM0-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA	602156887F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)	wt45g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'	Homo sapiens mRNA for KIAA1157 protein, partial cds	DNA TOPOISOMERASE III ALPHA	Homo sapiens mRNA for KIAA0905 protein, complete cds	SYNAPSIN II	SYNAPSIN II	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2) 2)	Homo sapiens Xq pseudœautosomal region; segment 1/2	yg33f12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34345 5'	RC1-BT0313-301299-012-f05 BT0313 Homo sapiens cDNA	z/36e09.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665512.5' similar to contains element MER22 reportition element:	Minister of the Company of the American Company of the	and sapiens Americal mixiva for Aine-1, complete cas	601655184K1 NIH_MGC_65 Home sapiens cDNA clone IMAGE:3845805 3	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMACE:3845805 3'	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
Top Hit Database Source	NT O	H	TN F N	L S				$\overline{}$	$\overline{}$	EST_HUMAN 6	SWISSPROT	EST_HUMAN w	Г	SWISSPROT D	H	SWISSPROT S	SWISSPROT S	NT (2)		EST_HUMAN M	EST_HUMAN R	Z Z LI MANI LI	NC NC	Т	\neg	EST_HUMAN 6	NT P	A	NT A
Top Hit Acession No.	U67922.1	X74463.1	AF064564.2	. ⊲	AE002324.2	AE002324.2	5453733 NT	AW900455.1	AW900455.1	BF681547.1	Q07869	AW054976.1	AB032983.1	Q13472	AB020712.1	Q92777	Q92777	AJ133269.1	AJ271735.1	R20459.1	BE064667.1	A A 4 OEE 200 4	AD000004	ı	3E962107.2	3E962107.2	U30790.1	U30790.1	AL161500.2
Most Similar (Top) Hit BLAST E Value	1.4E+00	1.4E+00	1.4E+00	1 4F+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1 45.00	1.1.00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00	1.4E+00
Expression Signal	9:38	1.63	3.29	3 20	1.01	1.01	0.87	1.09	1.09	1.53	8.0	1.51	5.17	2.39	6.4	2.71	2.71	1.86	5.21	1.88	3.37	70	1.94	4.97	5.15	5.15	2.68	2.68	1.34
ORF SEQ ID NO:		22394	22500	22504				23835	23836			25026		25812		25884	25885	26341		27325	27381.	200740	2007	C6997	28808	28809	28867	28868	
Exan SEQ ID NO:	1	12501	12608				13213	14062	14062	14376	15004	15222	15313	15702		15766	15766	16181	l	17133	17179	2000		\perp		18526	18583	18583	1 1
Probe SEQ ID NO:	2286	2634	2746	2746	3034	3034	3291	4162	4162	4482	5137	5301	5394	5796	5802	5860	2860	6318	7107	7256	7303	00,00	0440	8556	8709	8709	8727	8727	9221

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Top Hit Descriptor	M.mucedo gene encoding 4-Dihydromethyl-trisporate dehydrogenase	Cantharellus sp. partial 25S rRNA gene, isolate Tibet	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA	Coix lacryma-jobi dihydrodipicolinate synthase (dapA) gene, complete cds	Chlamydia muridarum, section 66 of 85 of the complete genome	Opprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP)	601661233R1 NIH MGC 72 Home sapiens cDNA clone IMAGE:3915945 31	Mus musculus alpha-spectrin 1. ervthroid (Spna1), mRNA	Fugurubribes gamma-aminobutvric acid receptor beta subtribit gene partial cds: 55kd envitrocyte membrane	protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase	enhancer protein (PCOLCE) genes, complete c>	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1	PM0-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA	PMo-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA	D.melanogaster no-on-transient A gene product, complete cds	Sus scrofa plp gene	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'	Homo sapiens GL004 protein (GL004), mRNA	Homo sapiens heparan glucosaminyi N-deacetylase/N-sulfotransferase-2 gene, complete cds	S.alba phr-1 mRNA for photofyase	S.alba phr-1 mRNA for photolyase	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID AI PHA-MANNOSIDASE) (I AMAN)	110 TO THE WAY OF THE WAY OF THE PROPERTY OF T	CONTROL NO CONTROL NOT IT TOURS SAPISES OF THE SINK OF LEGIS OF CONTROL SAFETY OF CO	60/163/143K1 NIT MGC_6/ HOM6 Sapiens CUINA CIONE IMAGE:3880193 3	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)	MRNA 3'-END PROCESSING PROTEIN RNA15
Top Hit Database Source	칟	NT	F			NT L	D .	5	\top	6755621 NT	✝	. Ω.	N H		NT	TN	EST_HUMAN P	T_HUMAN			T_HUMAN		H H		NT	TOGGSSIMS	7	7	ESI_HUMAN o	\neg	ヿ		SWISSPROT
Top Hit Acession No.	1.3E+00 Z73640.1	1.3E+00 AJ271192.1	Y19213.1	4507998 NT	4507998 NT	U61730.2	1.3E+00 AE002338.2		1.3E+00 RE966735.2	6755621			1.3E+00 AF016494.1	6755621 NT	1.3E+00 AJ252087.1	1.3E+00 AJ252087.1	1.3E+00 AW362834.1	4.1			1.3E+00 BE963379.2	9910247 NT	1.3E+00 AF042084.1	1.3E+00 X72019.1		000754	7	1		-			P25299
Most Similar (Top) Hit BLAST E Value	1.3E+00	1.3E+00	1.3E+00 Y	1.3E+00	1.3E+00	1.3E+00	1.3E+00	20.20	1.3E+00	1.3E+00			1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1 35+00 000754		1.35+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00 Q14117	1.3E+00 P25299
Expression Signal	1.67	2.74	16.5	10.9	10.9	1.62	2.09	Č	2.19	1.12			1.03	0.82	86.0	86.0	7.76	7.76	1.33	1.25	3.06	1.55	5.44	2.31	2.31	1 15	5 5	177	9.4	1.6	1.39	4.3	2.34
ORF SEQ ID NO:		20659		21033	21034			0		22632			23258	22632	24607	24608	25674	25675	25889	26901	26988			27560	27561	27630	27009	080/7	27751	27961	27968		28398
Exon SEQ ID NO:	10498	10810	11028	11183	11183	11241	11497		12378	12835			13463	12835	14839	14839	15576		15770		16795	16931	17350	17357	17357	4740E	72.11	1/4/1					18157
Probe SEQ ID NO:	929	884	1113	1275	1275	1334	1593	9070	2503	2909			3547	4502	4964	4964	2002	5665	5864	6828	6917	7054	7480	7487	7487	757.4	1 0001	070/	9/9/	7866	7874	8078	8277

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					9:9		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8299	18178	28424	2.23	1.3E+00	Z18892.2	TN	Mus musculus desmin gene
8646	18510		1.81	1.3E+00	1.1	EST_HUMAN	xp09e03.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739868 3'
8826	18639	28923	2.82	1.3E+00	D42042.1	IN	Human mRNA for KIAA0085 gene, partial cds
8895	18705	28999	2.71	1.3E+00	298682.1	IN	Bacillus subtilis genomic DNA 23.9kB fragment
9362	19033		2.35	1.3E+00	AF187873.1	NT	Gavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
9533	19139	25263	3.24	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158452 5'
9544	19499		2.68	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
634	10571	20384	8.14	1.2E+00	AA676246.1	EST_HUMAN	zi22d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
808	10735	20578	1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
908	10735		1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
808	10735	20580	1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
860	10786		2.19	1.2E+00	8924234 NT	TN	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1145	11058	20901	5.53		AF080245.2	N	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1187	11097	20943	1.77	1.2E+00	AJ252242.1	TN	pea seed-borne mosaic virus complete genome
1187	11097	20944	1.77	1.2E+00	AJ252242.1	F	pea seed-borne mosalc virus complete genome
1963	11857	21746	1.05	1.2E+00	AF140631.1	L	Homo sapiens G-profein coupled receptor 14 (GPR14) gene, complete cds
3072	12999	22789	0.95	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3128	13053	22851	5.41	1.2E+00	AL161563.2	NT	Arabidopsis thallana DNA chromosome 4, contig fragment No. 63
3128	13053	22852	5.41	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3249	13172		2.9	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3311	13232	23038	0.78	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3312	13233		0.99	1.2E+00	M81779.1	NT	G.gallus T-cadherin mRNA, complete cds
3650	13564	23350	7.28	1.2E+00	U75902.1	L/	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3904	13814	23598	1.49	1.2E+00	BF373570.1	EST_HUMAN	MR0-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4201	13232	23038	1.09	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4298	14196	23981	1.39	1.2E+00	TN 1560869	۲۷	Rattus norvegicus Glycine receptor alpha 2 subunit (glycine receptor, neonatal) (Glra2), mRNA
4371	14267		1.64	1.2E+00	M87060.1	TN	Rattus rattus cardiac AE3 gene, exons 1-23
4422	14316	24102	1.26	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4460	14354	24145	1.82	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4485	14379		5.44	1.2E+00	Y09200.1	NT	T.pinnatum chloroplast rbcL gene, partial
4284	13233		0.94	1.2E+00	M81779.1	NT	G.gallus T-cadherin mRNA, complete cds.
5409	15329			1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
5739	15647		2.47	1.2E+00	X74885.1		D.hydei ay1 repeat cluster DNA, fragment D
92/9	15676	25783	3.28	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA

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Top Hit Descriptor	C. glutamicum pta gene and ackA gene	C.glutamicum pta gene and ackA gene	ah84g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374.3'	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA	Mus musculus DSPP gene	AV734585 cdA Homo sapiens cDNA clone cdAAFH03 5'	Lilactis pyrD and pyrF genes	Homo sapiens mRNA for KIAA1204 protein, partial cds	MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA	R.communis gene for pyrophosphate-dependent phosphofructokinase beta subunit	HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01	H.sapiens ENO3 gene for muscle specific enolase	PM0-ST0264-161199-001-d01 ST0264 Homo sapiens cDNA	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds	Mus musculus 60 kDa ribonucleoprotein SSA/Ro gene, complete cds	Homo sapiens chromosome 21 segment HS21C003	Bacillus halodurans genomic DNA, section 9/14	Human mRNA for KIAA0227 gene, partial cds	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA	UI-HF-BR0p-ajk-f-02-0-UI.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'	Homo sapiens chromosome 21 segment HS21C013	Homo sapiens chromosome 21 segment HS210013	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to	SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1;	Xylella fastidiosa, section 32 of 229 of the complete genome	Xylella fastidiosa, section 32 of 229 of the complete genome	Homo sapiens calpain 9 (nCL-4) (CAPN9) mRNA	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA	R.unicornis complete mitochondrial genome	Drosophila melanogaster cytoplasmic dynein heavy chain mRNA, complete cds	African swine fever virus, complete genome
Top Hit Database Source	LN LN	F	EST_HUMAN	EST_HUMAN	F	EST_HUMAN	Z		EST_HUMAN		EST_HUMAN	IN	EST_HUMAN	EST_HUMAN	ĮN.	Z	<u> </u>	F	Z	EST_HUMAN	Г	뉟	Z	FN			T_HUMAN		NT .					ĮN.
Top Hit Acession No.	(89084.1	(89084.1	1.2E+00 AA759254.1	1.2E+00 AW813276.1	1.2E+00 AJ002141.1	1.2E+00 AV734585.1	(74207.1	1.2E+00 AB033030.1	1.2E+00 AW377210.1		011745.1	(56832.1	1.2E+00 AW817817.1	3E160761.1	J50147.1	1.2E+00 AF065398.1	4L163203.2	1.2E+00 AP001515.1	386980.1	1.1E+00 AW995393.1			4L163213.2	2641	8922973 NT		1.1E+00 AI808360.1	\E003886.1	NE003886.1	5729757 NT	8922641 NT	5835331 NT	23195.1	118466.1
Most Similar (Top) Hit BLAST E Value	1.2E+00 X89	1.2E+00 X89084.1	1.2E+00/	1.2E+00/	1.2E+00 /	1.2E+00/	1.2E+00 X74207.1	1.2E+00 /	1.2E+00	1.2E+00 Z32850.1	1.2E+00 D11745.1	1.2E+00 X56832.1	1.2E+00/	1.2E+00 BE	1.2E+00 U50147.1	1.2E+00 /	1.2E+00 AL1	1.2E+00	1.1E+00 D86980.1	1.1E+00	1.1E+00	1.1E+00/	1.1E+00 AL1	1.1E+00	1.1E+00		1.1E+00 /	1.1E+00 AE	1.1E+00 AE	1.1E+00	1.1E+00	1.1E+00	1.1E+00 L23195.1	1.1E+00 U18466.1
Expression Signal	1.87	1.87	32.83	1.82	2.55	1.9	2.4	3.45	1.74	3.08	1.8	3.28	. 2.03	23.47	4.87	2.5	15.4	1.49	1.13	1.39	0.92	6.61	6.61	0.93	1.26		0.99	1.16	1.16	17.81	0.99	5.89	1.18	2:92
ORF SEQ ID NO:	25815	25816	25841	. 25949	26121		26544	27055	27285	27480	27601	27786	28826		28145	28787	25067	-	20217	21496	21628	23009	23010	23165			23244	23357	23358	23378	23565		24520	24573
Exon SEQ ID NO:	15704	15704	15729	15823	15986	19463	16367	16861	17095	17274	17391	17561	18542	18576	17901	18877	19572	19025	10400	11627	11753	13209	13209	13358	13426		13447	13571	13571	13592	13773	14022	14740	14800
Probe SEQ ID NO:	5798	5798	5823	5918	6139	6369	6208	6984	7218	7407	7540	7711	8653	8689	8752	9114	9330	9349	456	1726	1857	3288	3288	3441	3510		3531	3657	3657	3678	3862	4122	4860	4921

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Probe (A) Expression (A) Most Similar (A) Most Similar (A) Most Similar (A) Top Hit Acession (A) Cop Hit (A) Publishes Source (A) Source (A) <th< th=""><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th></th<>								
4999 14874 24638 1.16 1.1E+00 X78426.1 NT 5249 16172 24945 1.57 1.1E+00 6978530 NT 5449 16370 25426 1.204 1.1E+00 6978530 NT 6420 16283 26444 1.39 1.1E+00 AL183682.1 EST_HUMAN 6422 16283 26444 1.93 1.1E+00 AL183682.1 NT 6425 16286 26458 7.53 1.1E+00 AL181862.1 NT 6436 16286 26468 7.53 1.1E+00 AL161688.2 NT 6436 17584 27733 1.66 1.1E+00 AL161688.2 NT 7744 17584 27815 2.08 1.1E+00 AL161618.2 NT 8043 1734 28182 2.41 1.1E+00 AL61618.2 NT 8044 1734 2.08 1.1E+00 AL60694.1 NT 8043 1784 2.88 1.1E+00	Probe SEQ ID NO:			Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5249 157 1.1E+00 G978500 NT 5449 1537 24945 1.57 1.1E+00 BE660184.1 EST HUMAN 6460 15380 25440 1.29 1.1E+00 AL18582.1 EST HUMAN 6422 16283 25444 1.29 1.1E+00 AL18582.1 NT 6425 16286 2648 7.83 1.1E+00 AL22338.1 NT 6435 16286 26789 3.22 1.1E+00 AL72338.1 NT 6472 1650 27733 1.65 1.1E+00 AL616188.2 NT 774 1756 27731 1.65 1.1E+00 AL61618.2 NT 774 17584 27815 2.03 1.1E+00 AL61618.2 NT 8043 1763 27815 2.04 1.1E+00 AL61618.2 NT 8447 1832 28581 4.41 1.1E+00 AL608942.1 NT 8652 18551 28885 4.41 <td< td=""><td>4999</td><td></td><td></td><td></td><td>1.1E+00</td><td>18425.1</td><td>NT</td><td>E.faecalis pbp5 gene</td></td<>	4999				1.1E+00	18425.1	NT	E.faecalis pbp5 gene
5449 15370 25426 1.204 1.1E+00 BE960184.1 EST HUMAN 6420 15380 25440 1.29 1.1E+00 Al138582.1 EST HUMAN 6422 16283 25444 1.39 1.1E+00 Z7238.1 NT 6422 16283 25445 1.39 1.1E+00 Z7238.1 NT 6436 16296 27458 2.53 1.1E+00 AL161582.2 NT 7658 1760 27733 1.65 1.1E+00 AL161516.2 NT 7744 17594 27731 1.65 1.1E+00 AL061516.2 NT 7744 17594 27815 2.0.08 1.1E+00 AL06156.2 NT 8043 1784 1.1E+00 AF06342.1 NT NT 8450 18851 2.44 1.1E+00 AF06864.2 NT 8450 18823 2882 4.41 1.1E+00 AF06864.1 NT 8450 18823 2882 <t< td=""><td>5249</td><td></td><td></td><td></td><td>1.1E+00</td><td>6978530</td><td>Ŋ</td><td>Rattus norvegicus Aquaporin 4 (Aqp4), mRNA</td></t<>	5249				1.1E+00	6978530	Ŋ	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
6420 15380 25440 1.29 1.1E+00 Z72338.1 EST_HUMAN 6422 16283 25444 1.93 1.1E+00 Z72338.1 NT 6422 16283 25445 1.93 1.1E+00 Z7238.1 NT 6435 16283 25468 7.63 1.1E+00 BF8328.1 NT 7744 17504 27731 4.39 1.1E+00 AL023151.1 NT 7744 17594 27815 2.08 1.1E+00 AL023151.1 NT 8043 17981 2.781 2.08 1.1E+00 AL02342.1 NT 80447 17834 28182 2.66 1.1E+00 AF012862.1 NT 8045 18323 28581 4.41 1.1E+00 AF012862.1 NT 8046 18323 28581 4.41 1.1E+00 AF012862.1 NT 8047 18329 4.41 1.1E+00 AF012862.1 NT 8048 18323 2	5449				1.1E+00	BE960184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'
6422 16283 26444 1.98 1.1E+00 Z7238.1 NT 6422 16283 26445 1.93 1.1E+00 Z7238.1 NT 6436 1626 26465 7.53 1.1E+00 Z72338.1 NT 6436 1626 26468 7.53 1.1E+00 A165386.1 EST_HUMAN 7658 17608 27733 1.65 1.1E+00 AL65316.1.1 NT 774 17544 27781 2.05 1.1E+00 AL65316.1.1 NT 8043 17834 28182 2.65 1.1E+00 AL067364 NT 8047 17834 28182 2.65 1.1E+00 AL067364 NT 8047 17834 28182 2.41 1.1E+00 AL067364 NT 8047 17834 28182 4.41 1.1E+00 AL063629.1 NT 8047 18829 3.41 1.1E+00 AF068942.1 NT 8052 18829 4.41 <td>5460</td> <td>\Box</td> <td>L</td> <td>1.29</td> <td>1.1E+00</td> <td></td> <td>EST_HUMAN</td> <td>qd85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736260 3'</td>	5460	\Box	L	1.29	1.1E+00		EST_HUMAN	qd85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736260 3'
16283 26445 1.93 1.1E+00 Z7233.1 NT 16296 26468 7.53 1.1E+00 AL161588.2 NT 17508 27733 1.65 1.1E+00 AB023151.1 NT 17564 27731 1.65 1.1E+00 AB023151.1 NT 17564 27791 4.39 1.1E+00 AB023151.1 NT 17584 27815 2.0.08 1.1E+00 AF0421 NT NT 17842 27815 2.0.08 1.1E+00 AF042862.1 NT 18323 28581 4.41 1.1E+00 AF012862.1 NT 18551 28582 4.41 1.1E+00 AF012862.1 NT 18599 4 1.1E+00 AF012862.1 NT 19056 25310 2.13 1.1E+00 AF012862.1 NT 19070 25310 2.13 1.1E+00 AF012862.1 NT 10071 3.49 1.1E+00 AF01689.1 NT	6422			1.93	1.1E+00		N	Herpes simplex virus type 1 (strain KOS) UL41 gene
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Page 18 of 413 Table 4 Single Exon Probes Expressed in Heart

בוויים ביים ביים ביים ביים ביים ביים ביי	Top Hit Descriptor	Mus musculus Serf1 protein (Serf1), survival of motor neuron protein (Smn), neuronal apoptosis inhibitory protein-rs6 (Naip-rs6), and neuronal apoptosis inhibitory protein-rs3 (Naip-rs3) genes, complete cds	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)	HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME I	af26g08.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:C42DB.3 CE04204 ;contains element MER22 MER22 repetitive element ;	Rattus norvegicus neuromedin U precursor (NmU) gene, exons 5 and 6	Xenopus laevis rhodopsin gene, complete cds	Agaricus bisporus mRNA for tyrosinase	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively	Balliced	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA	Taenia ovis 45W antigen (ToW4) gene, complete cds	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds	Bacillus subtilis 42.7kB DNA fragment from yvsA to yvqA	Hordeum vulgare gene encoding cysteine proteinase	Bos taurus micromolar calcium activeted neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	FIBER PROTEIN	UI-H-BIS-alx-d-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE)	(BL-CAM)	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds	ac79b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868791 3'	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
אוכן דייסון ו	Top Hit Database Source	TN TN	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN \	IN.	() IN	N IN					J LN	N F	INT	NT	NT	SWISSPROT	EST_HUMAN	IN LN		ISSPROT	T			_ HUMAN	NT.
5	Top Hit Acession No.	AF131205.1	P24008	P24008	014226	AA628453.1	AF222761.1	U23808.1	AJ223816.1	7 7000001	AFZZ3391.1	8922245 NT	U75741.1	D10852.1	AJ223978.1	Z97022.1	AF248054.1	AF248054.1	P04501	AW452782.1	U75902.1		P20273	AF192531.1	AA775191.1	1.0E+00 BE868267.1	ш,	D10852.1
	Most Similar (Top) Hit BLAST E Value	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00		1.05+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00		1.0E+00 P20273	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
	Expression Signal	1.09	3.48	3.48	0.99	1.17	0.81	1.15	1.44		0.80	0.79	0.88	0.88	0.87	2.49	4.31	4.31	4.82	1.39	2.21		8.43	1.34	5.99	1.71	1.71	1.38
	ORF SEQ ID NO:	22408	22561	22562		22891			23328	00000	73660				24777	24919	25557	25558	25729	25730	25939			26574	26583	26713	26714	
	Exon SEQ ID NO:	12518	12774		12865	13087	13247	10077	13541	1000	- [14078	14698	14828	15006	15152	15484	15484	15626	15627	15814		16279	- (16404	1	- 1	14828
	Probe SEQ ID NO:	2651	2846	2846	2938	3162	3327	3548	3627	000	R/68	4178	4815	4951	5139	5228	5568	5568	5719	5720	2908		6417	6537	6546	6641	6641	6734

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						_	_	_	_	_		_			_			_	_	_		_	_	_		_	_	_	
	Top Hit Descriptor	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]	RC1-HT0229-181099-011-e06 HT0229 Homo sapiens cDNA	Human immunodeficiency virus type 1 (HIV-1), Isolate SF33,	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA	AV689554 GKC Homo sapiens cDNA clone GKCCYA11 51	Xenopus laevis zona pellucida C glycoprotein precursor (xiZPC) mRNA, complete cds	Xenopus laevis zona pellucida C glycoprotein precursor (xIZPC) mRNA, complete cds	AV758825 BM Homo sapiens cDNA clone BMFAW C04 5'	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)	EST388293 MAGE resequences, MAGN Homo saplens cDNA	Homo sapiens mRNA for KIAA1517 protein, partial cds	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C102	Apple mosaic virus RNA 2 putative polymerase gene, complete cds	SERINE/THREONINE PROTEIN KINASE MINIBRAIN	Lycopersicon esculentum putative Mi1 copy 1 nematode-resistance gene	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'	601653563R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL- like protein, isolate JM983
	Top Hit Database Source	SWISSPROT	SWISSPROT	EST_HUMAN		EST_HUMAN	INT	IN	EST_HUMAN	IN	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	TN	N L	TN	NT	TN	SWISSPROT	TN	SWISSPROT	TN	SWISSPROT	EST_HUMAN	EST_HUMAN	N
	Top Hit Acession No.	Q02207	002207	1.0E+00 BE147331.1	1.0E+00 M38427.1	1.0E+00 BE907592.1	6753429 NT	6753429 NT	1.0E+00 AV689554.1	1.0E+00 U44952.1	1.0E+00 U44952.1	1.0E+00 AV758825.1	1.0E+00 AA004982.1	1.0E+00 AA004982.1	P15306	1.0E+00 AW976184.1	1.0E+00 AB040950.1	9.9E-01 AF245455.1	9.9E-01 AF245455.1	9.9E-01 AL163302.2	9.9E-01 AF174585.1	P49657	9.9E-01 U65667.1	9.9E-01 Q28642	9.9E-01 AJ005029.1	P22567	9.8E-01 BE957439.2	9.8E-01 BE957439.2	9.8E-01 AJ302158.1
Most Similar	(Top) Hit BLAST E Value	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00 P15306	1.0E+00	1.0E+00	9.9E-01	9.9E-01	9.9E-01	9.9E-01	9.9E-01 P49657	9.9E-01	9.9E-01	9.9E-01	9.8E-01 P22567	9.8E-01	9.8E-01	9.8E-01
	Expression Signal	2.7	2.7	2.01	1.9	1.76	1.28	1.28	2.03	1.2	1.2	2.83	17.08	17.08	2.05	1.51	1.67	0.84	0.84	6.0	1.18	9.22	1.38	2.43	2:92	2.32	0.82	0.82	4.61
	ORF SEQ ID NO:	26932	26933	l	27133	27405		27527		27609	L	28005	28075	28076				21315		22360		25441			28237	20265	23429	23430	26292
	Exon SEQ ID NO:	16740	16740	19466	16941	17207	17320	17320	17395	17397	17397	17766	17835	17835	18928	19126	19350	11458	11458	12467	13468	15381	17204	17298	17988	10454	13644	13644	16137
	Probe SEQ ID NO:	6861	6861	2969	7064	7339	7460	7460	7544	7546	7546	7916	7985	7985	9193	9513	6986	1553	1553	2598	3553	5461	7336	7510	8097	512	3732	3732	6272

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יייין ויייין אייין איין אייין אייין אייין אייין אייין אייין אייין אייין אייין איין אייין איין אי	Top Hit Descriptor	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL- like protein, isolate JM983	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'	601110258F1 NIH_MGC_16 Homo sepiens cDNA clone IMAGE:3350750 5	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >	we52e04.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2345694.3'	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)	UI-H-BI4-aci-e-07-0-UI,s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds	PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA	Homo sapiens KIAA0914 gene product (KIAA0914), mRNA	Parvovirus B19 DNA, patient C, genome position 2448-2994	Parvovirus B19 DNA, patient C, genome position 2448-2994	P.falciparum complete gene map of plastid-like DNA (IR-A)	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial	protein, partial cds	601675539F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5	RC1-CT0295-241199-011-b02 CT0295 Homo sapieris cDNA	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds	601466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869929 5	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA	Homo sapiens phytanoyi-CoA hydroxylase (PHYH) gene, exon 5
מסו ווסעיין סול	Top Hit Database Source	<u> </u>	EST_HUMAN	EST_HUMAN	Ż	T_HUMAN		F	F	EST_HUMAN		TN	IN	EST_HUMAN		F	TN			EST_HUMAN /	-			EST_HUMAN (EST_HUMAN		I	EST_HUMAN (
	Top Hit Acession No.	AJ302158.1	3E258705.1	3E258705.1	J52111.2	AI660384.1	J26716.1	4F149112.1	M90544.1	3F511209.1	AL114281.1	4F197925.1	4F197925.1	4W799674.1	7662375 NT	270556.1	270556.1		4V752605.1	4V752605.1			3E902340.1	3E902340.1	4W861102.1	4F165990.1	4F080595.1	BE781251.1	11419857 NT	AF242382.1
	Most Similar (Top) Hit BLAST E Value	9.8E-01	9.8E-01	9.8E-01	9.8E-01	9.7E-01	9.7E-01	9.7E-01	9.7E-01	9.7E-01	9.7E-01	9.6E-01	9.6E-01	9.6E-01	9.6E-01	9.6E-01	9.6E-01	9.6E-01	9.6E-01	9.6E-01		9.6E-01	9.5E-01	9.5E-01	9.5E-01	9.4E-01	9.4E-01	9.4E-01	9.4E-01	9.3E-01
	Expression Signal	4.61	4.43	4.43	1,62	1.01	2.37	1.86	1.74	4.52	1.39	8.9	6.8	1.3	0.92	3.46	3.46	1.37	4.15	4.15		1.52	1.6	1.6	1.17	3.37	1.67	1.64	1.43	1.11
	ORF SEQ ID NO:		28487	28488			26266	27023	27025			24016	. 24017	24036	24729	25498	25499		28912	28913			23410	23411	27336					
	Exon SEQ ID NO:	16137	18239	18239	19061	14974	16114	16830	16832	18382	19419	14234	14234	14251	14953	15435	15435	16769	18622	18622		- 1		13627	17143	13090	13106	19029	19564	11601
	Probe SEQ ID NO:	6272	8362	8362	9408	5106	6248	6952	6954	8510	9926	4337	4337	4355	5083	5517	5517	06890	8088	8808		9709	3715	3715	7266	3165	3181	9354	9708	1700

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	Top Hit Descriptor	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA	Bovine papillomavirus type 2, complete genome	Bovine papillomavirus type 2, complete genome	Equus caballus microsatellite LEX013	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds	oe09b03.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357	Aedes triseriatus putative large subunit ribosomal protein rpL34 mRNA, complete cds	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B); melanoma antigen family A3 (MAGEA3), caltractin (CALT). NAD(P)H dehydrogenase-like protein (NSDHL), and LI>	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864661 5	Mus musculus carbonic anhydrase 4 (Car4), mRNA	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA	7058e06.X1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5;	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5	602154769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295896 5'	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'	Rattus norvegicus mucin (MUC2) gene, partial cds	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)	ob71g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336862 3'	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA	Homo sapiens neurexin III-alpha gene, partial cds	Oryctolagus cuniculus Rad51 (RAD51) mRNA, complete cds	Xenopus laevis gene for aldolase, complete cds
-	Top Hit Database Source	EST_HUMAN R	N B	N N	NT	TN FN	S IN	EST_HUMAN @		H 8 9	T HUMAN	EST_HUMAN 6			FST_HUMAN P	EST_HUMAN 6			EST_HUMAN_A	EST_HUMAN A	NT	SWISSPROT IN		NT R	H				×
	Top Hit Acession No.	9.3E-01 BE071172.1	9.3E-01 M20219.1		9.3E-01 AF075615.1	9.3E-01 AF213884.1	9.3E-01 L36189.1	1			9.2E-01 BE622702.1	_	6671677 NT	11430963 NT	9.2E-01 BF593251.1		9.2E-01 BF680047.1	8923056 NT	126418.1	T26418.1	9.1E-01 U68172.1		23.1		9.1E-01 AF050113.1	7661625 NT	9.0E-01 AF099810.1	1.	9.0E-01 D38621.1
	Most Similar (Top) Hit BLAST E Value	9.3E-01	9.3E-01	9.3E-01	9.3E-01	9.3E-01	9.3E-01	9.3E-01	9.3E-01	9.3E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.1E-01	9.1E-01 T	9.1E-01	9.1E-01	9.1E-01 Q61704	9.1E-01	9.1E-01	9.1E-01	9.0E-01	9.0E-01	9.0E-01	9.0E-01
	Expression Signal	1.13	0.82	0.82	1.54	1.62	3.84	1.88	1.56	1.38	3.04	4.23	1.38	3.63	1.73	1.85	2.01	1.43	0.97	0.97	0.86	2.92	15.99	2.2	30.05	0.89	2.37	0.82	1.45
-	ORF SEQ ID NO:	22357	23630	23631		25410	25465	26771					27688	27983	28041	29059	29101		22898	22899	23991	25950	26498	26587		22900	23959	24589	
	Exon SEQ ID NO:	l	13857	13857	15022	15354	15402	16581	19325	19418	13125	15556	17469	17740	17802	18767	18809	11967	13094	13094	14207	15824	16331	16409	19641	13095	ii		16250
	Probe SEQ ID NO:	2594	3949	3949	5155	5434	5482	6701	9822	9954	3201	5643	7618	7890	7952	8960	9006	2077	3169	3169	4310	5919	6472	6551	9445	3170	4282	4945	6388

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- '		_	_	_		_							_										_	_	_		_			_		
Top Hit Descriptor	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>	Rabbit MHC fragment RLA-DF DNA	Xylella fastidiosa, section 90 of 229 of the complete genome	Chlamydophila pneumoniae AR39, section 21 of 94 of the complete genome	PUTATIVE F420-DEPENDENT NADP REDUCTASE	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643	Homo sapiens SOS1 (SOS1) gene, partial cds	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA	nn05f11.s1 NCI_CGAP_Pr4.1 Homo sapiens cDNA clone IMAGE:1076877	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-	halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2- dioxygenation of the ISP protein OhbB (حالم) عبداً المراكبة المراكب	dioxygalase apriator proteir Oribb (Oribb), and pur	Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'	AV661898 GLC Homo sapiens cDNA clone GLCGYG07 3'	Rat IGFII gene for insulin-like growth factor II	zd44e03.r1 Scares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343516 5'	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous	xantromatosis), potypeptide 1 (CTFZ/ATB) mNVA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds	Chicken lipoprotein lipase gene	Chicken lipoprotein lipase gene	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds	Bacillus halodurans genomic DNA, section 12/14	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'	Cyanidium caldarium gene for SigC, complete cds	Cyanidium caldarium gene for SigC, complete cds
Top Hit Database Source		NT	N	NT				TN	NT	T_HUMAN					EST_HUMAN	EST_HUMAN	EST_HUMAN	Г	NT	EST_HUMAN				IN	LN	Ŋ	N	NT	NT	EST_HUMAN		NT
Top Hit Acession No.	4F026198.1	X60986.1	8.9E-01 AE003944.1	8.9E-01 AE002186.2			8.8E-01 D90911.1	8.7E-01 AF106953.2	5901893 NT	8.7E-01 AA595863.1				8.7E-01 AE004963.1	8.7E-01 BF363970.1	8.7E-01 BF107694.1	8.7E-01 BF107694.1	8.7E-01 AV661898.1	X17012.1	8.6E-01 W69089.1	0740027	4503Z10[N]	8.6E-01 AL161565.2	49724.1	60547.1		8.6E-01 AF143732.1	4F143732.1	AP001518.1			8.5E-01 AB006799.1
Most Similar (Top) Hit BLAST E Value	8.9E-01	8.9E-01	8.9E-01	8.9E-01	8.8E-01 O26350	8.8E-01	8.8E-01	8.7E-01	8.7E-01	8.7E-01		16	8.75-01	8.7E-01	8.7E-01	8.7E-01	8.7E-01	8.7E-01	8.6E-01	8.6E-01	100	8.0E-01	8.6E-01	8.6E-01	8.6E-01 X	8.6E-01 X	8.6E-01	8.6E-01	8.6E-01	8.5E-01	8.5E-01	8.5E-01
Expression Signal	2.08	1.32	3.47	4.74	3.28	2.98	1.75	1.54	1.09	4.64		0	7:31	1.45	5.47	4.16	4.16	2.78	1.66	3.62	,	1.01	0.81	1.29	11.82	11.82	2.14	2.14	1.52	2.75	1.36	1.36
ORF SEQ ID NO:	25476	ý	29085			28560		20218		22560										20618				23427			26065				28013	
Exon SEQ ID NO:		15692	18794	18987			19722	10401	12233	L						18776	18776	19534	10409	10767		12109				15509	15934	L			L	
Probe SEQ ID NO:	5494	2186	8990	9285	4442	8430	9108	457	2353	2845		7	4938	7613	8206	8970	8970	9488	466	840		577.4	3568	3730	5595	5695	9030	6030	6626	6443	7924	7924

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	Top Hit Descriptor	Homo sapiens human immunodeficiency virus type I enhancer-binding protein 1 (HIVEP1), mRNA	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Pton5), mRNA	Mus musculus mper1 gene for period1, complete cds	Mus musculus NK cell receptor 2B4 gene, promoter region and partial cds	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7	Pyrococcus abyssi complete genome; segment 5/6	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds	Arabidopsis thallana DNA chromosome 4, contig fragment No. 18	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds	Streptomyces antibioticus polyketide biosynthetic gene cluster	Canis familiaris MHC DLA Class II DRB pseudogene DRB2	Canis familiaris MHC DLA Class II DRB pseudogene DRB2	Canis familiaris MHC DLA Class II DRB pseudogene DRB2	Canis familiaris MHC DLA Class II DRB pseudogene DRB2	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40	nn01f12.y5 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.t1 THR	repetitive element;	Drosophila melanogaster Lis1 homolog mRNA, complete cds	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the	Objects genome	Triyophinina ilicatans miloononantini, oonipiete gandina	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5	Rattus norvegicus mRNA for RPHO-1, complete cds	Mus musculus trophinin (Tnn) gene, complete cds	IL3-CT0219-161199-031-C08 CT0219 Homo saplens cDNA	Rattus norvegicus mRNA for RPHO-1, complete cds	CM/4-HT0243-08/199-037-e01 HT0243 Homo sapiens cDNA	S.cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-Isoproplymalate (alpha-IPM)	synthetase (partial), and DNA polymerase alpha (partial) Homo ceniens thincolovin-related protein mBNA complete ode	and sapiens uniquedoni rietated protein minnay, complete cas	MCKUSICK-KAUFMANIBARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
-	Top Hit Database Source			NT TN	NT							NT	NT		NT		NT A		T_HUMAN		N N				H		N FA	EST_HUMAN IL		EST_HUMAN C		E L		SWISSPROT. IN
	Top Hit Acession No.	11418543 NT	TN 8007008	AB030818.1	F143509.1	78726.1				8.3E-01 AL161506.2			J46916.1	J46916.1	J46916.1	J46916.1	8.3E-01 AL161540.2					7 000000	AE000903.1	12147171		8.2E-01 AB000489.1		_		AW379433.1			6.ZE-U1 ArU3Z639.1	
	Most Similar (Top) Hit BLAST E Value	8.5E-01	8.5E-01	8.5E-01	8.4E-01	8.4E-01	8.4E-01	8.4E-01	8.3E-01	8.3E-01	8.3E-01	8.3E-01 Y	8.3E-01	8.3E-01	8.3E-01	8.3E-01	8.3E-01		8.3E-01	8.3E-01	8.3E-01	70.0	טייט ויס	0.00	8.3E-01	8.2E-01	8.2E-01	8.2E-01	8.2E-01	8.2E-01		8.2E-01 212126.1	0.ZE-U1	8.2E-011
	Expression Signal	2.52	2.63	1.29	0.84	2.7	2.7	3.13	2.31	2.64	1	3.11	1.12	1.12	0.95	0.95	2.13		4.2	1.23	3.1	07.0	2,40	2.40	2.03	2.99	1.51	1.14	1	3.26		3.58	SC:	6.66
	ORF SEQ ID NO:			25243	23785	25145	25146		20486	22774	23434	23619	24570	24571	24570	24571	24839			27914	27962	70000	40707		28760	21789	-		24691	26154			1./9/7	28028
	Exon SEQ ID NO:	19643	19075	19238	14008			17571	10656	12983		13839	14796	14796	14796	14796	15145		17424	17672	17717		1,905	١.,	18488		11934	1		16016	İ	- 1	-1	17787
	Probe SEQ ID NO:	9430	9436	9683	4108	5378	5378	7721	724	3056	3739	3930	4917	4917	5177	5177	5222		7573	7822	7867	0000	2000	0/00	8623	2006	2043	2646	5045	6122		6308	8	7937

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	Top Hit Database Source	SWISSPROT MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN	NT Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA	SWISSPROT OVARIAN TUMOR LOCUS PROTEIN	w/14d02.r1 Soares, placenta, 8to9weeks, 2NbHP8to9W Homo sapiens cDNA clone IMAGE:252195 5' EST HUMAN similar to ab:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);	NT Mus musculus mRNA for NIPSNAP2 protein	Т	NT Homo sapiens MHC class 1 region	NT Homo sapiens MHC class 1 region	SWISSPROT NEURONAL MEMBRANE GLYCOPROTEIN MG-B	SWISSPROT NEURONAL MEMBRANE GLYCOPROTEIN MG-B	EST_HUMAN RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA		NT Thermotoga maritima section 23 of 136 of the complete genome	NT Staphylococcus aureus partial pta gene for phosphate actyltransferase allele 15	NT Bos taurus futb and rtlf genes	EST_HUMAN 602072473F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215091 5'		NT Mus musculus gene for oviductal glycoprotein, complete cds	,	NT G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit	EST_HUMAN RC0-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA					NT Oryctolagus cuniculus mRNA for mitsugumin29, complete cds		NT Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds	EST_HUMAN 601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'	6753745 NT Mus musculus embigin (Emb), mRNA			NT S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
'	Top Hit Acession No.	Q9JI70	8.2E-01 L10127.1	P10383	H87398.1	8.2E-01 AJ001261.1	8.1E-01 AF191839.1	8.1E-01 AF055066.1	8.1E-01 AF055066.1	Q13491	Q13491	BE938558.1	8.1E-01 BE938558.1	8.1E-01 AE001711.1	8.0E-01 AJ271510.1	8.0E-01 AJ132772.1	8.0E-01 BF530962.1	8.0E-01 AF127897.1	8.0E-01 AB006193.1	8.0E-01 AL162758.2	X83739.2	8.0E-01 AW901489.1	7.9E-01 D11476.1	7.9E-01 AE002130.1	7.9E-01 AB040885.1	U32739.1	AB004816.1	7.9E-01 AF130459.1	7.9E-01 AF228664.1	7.9E-01 BE263612.1	67537		7.9E-01 Z47210.1	7.9E-01 Z47210.1
	Most Similar (Top) Hit BLAST E Value	8.2E-01 Q9JI70		8.2E-01 P10383	8.2E-01	8.2E-01	8.1E-01	8.1E-01	8.1E-01	8.1E-01 Q13491	8.1E-01 Q13491	8.1E-01			8.0E-01			8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01			7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01
	Expression Signal	99.9	2.81	9	6.65	1.73	1.29	2.81	2.81	2.49	2.49	1.94	1.94	1.84	3.02	3.76	1.83	2.73	1.14	1.8	5.65	2.84	3.78	1.16	65.97	1.37	5.24	2.29	2.75	0.92	1.02	1.02	0.84	0.84
	ORF SEQ ID NO:	28029	29011	. 29064	29069	25284		23130	23131	26020	26021	28879	28880	25343		20070		22761	22993		24115		20211		!		22006	22007			24188	24189		24721
	Exan SEQ ID NO:	17787	18717	18772	18777	19083	12593	13329	13329	15897	15897	18592	ı	18909	10142	10250		12967	13194	L	14327	16541	10390	10631	11491	11538	12102	12103	13388	14103	14401	14401	ı	14945
	Probe SEQ ID NO:	7937	8909	9968	8971	9451	2731	3412	3412	5992	5992	8775	8775	9166	170	285	1990	3039	3273	3643	4432	6661	446	869	1587	1634	2216	2217	3472	4204	4508	4508	5075	5075

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_				_								_									_	_						_				
	Top Hit Descriptor	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17	P.sativum GR gene	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds	SMALL HYDROPHOBIC PROTEIN	Homo sapiens KIAA1072 protein (KIAA1072), mRNA	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04	EST371637 MAGE resequences, MAGF Homo sapiens cDNA	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds	Sphenodon punctatus alpha enolase mRNA, partial cds	D.discoideum racGAP gene	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds	Mus musculus major histocompatibility locus class II règion; major histocompatibility protein class II alpha	chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds,	butyrophilin-like (NG9), butyrophilin-li>	CITRATE SYNTHASE	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7	(Callyac-17) (GALIYAC-17), MANA	Homo sapiens PRO1975 mRNA, complete cds	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds	RAFFINOSE INVERTASE (INVERTASE)	RAFFINOSE INVERTASE (INVERTASE)	yf24b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3'	Alacheman Alacheman (Al COA) item data assess and median advantage of the COA and the self assessment.	Lycopersicon misuum ADT-gucose pyrophosphoryrase large subunit (AGT-L.1) mKNA, complete cas	Archaeoglobus fulgidus, complete genome	Arabidopsis thallana 3-methylorotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete	spo	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
	Top Hit Database Source	NT	NT	N	SWISSPROT	님	SWISSPROT	EST_HUMAN	EST_HUMAN	NT	NT	LN LN	NT TA	LN			Z	SWISSPROT	ŀ		LN	NT	LN	SWISSPROT	SWISSPROT	EST_HUMAN	Ŀ	I.V.	NT		N	IN
	Top Hit Acession No.	7.9E-01 M29930.1	7.9E-01 X90996.1	U01912.1	P19719	7662471 NT	P19022	7.8E-01 Z43785.1	7.8E-01 AW959567.1	U87305.1	AF115856.1	Y10159.1	L29260.1	7.7E-01 AF184345.1			7.7E-01 AF050157.1	033915		N 8045858	AF118085.1	7.7E-01 AF199488.1	7.7E-01 AF199488.1	P16553	P16553	7.7E-01 R08600.1	7 17 07 07 1	7.7E-01 AF184345.1	11497621 NT		AF059510.1	7.6E-01 AF059510.1
	Most Similar (Top) Hit BLAST E Value	7.9E-01	7.9E-01	7.9E-01 U	7.9E-01 P19719	7.9E-01	7.9E-01 P19022	7.8E-01	7.8E-01	7.8E-01	7.8E-01	7.8E-01	7.8E-01	7.7E-01			7.7E-01	7.7E-01 033915	ļ	7.7=-01	7.7E-01 AF	7.7E-01	7.7E-01	7.7E-01 P16553	7.7E-01 P16553	7.7E-01	ļ	/./E-01	7.7E-01		7.6E-01 A	7.6E-01
	Expression Signal	1.01	2.43	4.78	3.95	2.36	2.48	1.75	3.2	0.79	2:32	1.27	1.42	6.33			1.85	2.8		S.	4.45	2.88	2.88	1.44	1.44	1.95		2.0	6.14		4.04	4.04
	ORF SEQ ID NO:		26790		27864		28682		L	24278	25709	27399		19932				22436								25630		19932			25720	25721
	Exon SEQ ID NO:	14954	16601	17373	17631	18249	18415	10784	12114	14491	15607	17199	19623	10112			10641	12545			_	14195	14195		15335	15541			19004		15618	15618
	SEQ ID NO:	5084	6721	7504	7781	8372	8543	828	2229	4603	5698	7323	9424	138			709	2680		3373	3549	4297	4297	5415	5415	5626	970	3717	9311		5710	5710

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Top Hit Descriptor	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds	Mus musculus advillin (Advil-pending), mRNA	Mus musculus advillin (Advil-pending), mRNA	Mus musculus cytochrome P450, 2b9, phenobarbitol inducible, type a (Cyp2b9), mRNA	MUSCARINIC ACETYLCHOLINE RECEPTOR M2	MUSCARINIC ACETYLCHOLINE RECEPTOR M2	H.aspersa mRNA for neurofilament NF70	H.aspersa mRNA for neurofilament NF70	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88	Homo sapiens mRNA for KIAA0895 protein, partial cds	Homo sapiens chromosome 21 segment HS21C101	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5	C14203 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-037E11 5'	Homo sapiens hypothetical protein FLJ10793 (FLJ10793), mRNA	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome	tr14b09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu	repetitive element,contains element MIR repetitive element;	Homo sapiens mRNA for KIAA0534 protein, partial cds	Malva pusilla actin (Act1) mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C046	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'	Mus musculus complement component 1 inhibitor (O1nh), mRNA	ta13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'	Borrelia burgdorferi (section 52 of 70) of the complete genome	Homo sapiens HT017 mRNA, complete cds	Homo sapiens growth arrest-specific 7 (GAS7), transcript variant b, mRNA	Mus musculus antigen (CD72) gene	Mus musculus antigen (CD72) gene
Top Hit Database Source	ŢN	ᅜ	TN	NT		SWISSPROT	NT	TN	TN	NT	NT	IN	EST_HUMAN	NT	NT	NT	Ł		T HUMAN	NT	IN	NT	EST_HUMAN	NT	EST_HUMAN	NT	NT	NT	뉟	NT
Top Hit Acession No.	AF146793.2	6857752 NT	6857752 NT	6753577 NT			86347.1	7.6E-01 X86347.1	7.6E-01 AL161592.2	7.6E-01 AB020702.1	7.5E-01 AL163301.2	7.5E-01 AF020503.1	7.5E-01 C14203.1	8922672 NT	7.5E-01 AF163151.2	7.5E-01 D90907.1	7.5E-01 AE000823.1		7.4E-01 AI598146.1	7.4E-01 AB011106.1	7.4E-01 AF112538.1	7.4E-01 AL163246.2	BE747503.1	6753217 NT	7.4E-01 AI472641.1	7.3E-01 AE001166.1	7.3E-01 AF225421.1	5360211 NT	L35772.1	L35772.1
Most Similar (Top) Hit BLAST E Value	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01 P30372	7.6E-01 P30372	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.5E-01	7.5E-01	7.5E-01	7.5E-01	7.5E-01	7.5E-01	7.5E-01		7.4E-01	7.4E-01	7.4E-01	7.4E-01	7.4E-01	7.4E-01	7.4E-01	7.3E-01	7.3E-01	7.3E-01	7.3E-01 L	7.3E-01 L
Expression Signal	1.41	2.04	2.04	1.28	7.52	7.52	2.31	2.31	4.81	2.74	1.52	2.23	0.88	13.92	3.57	1.87	1.42		1.23	0.97	1.22	4.43	7.23	3.28	1.59	0.95	4.76	1.1	5.61	5.61
ORF SEQ ID NO:	26770	26796	26797	27252	27414	27415	28837	28838				20315	23040	19900		25209	25190		20869	22076	23366	23889	27328			24194	24277		26010	
Exon SEQ ID NO:	16579	16606	16606	17061	17215	17215	18553	18553	18756	18850	10444	10508	13236	10083	19042	19329	19368	,	11029	12177	13579	14111	17135	18828	18901	14408	14490	14994		15889
Probe SEQ ID NO:	6699	6726	6726	7184	7347	7347	8664	8664	8948	9073	502	569	3315	4573	9381	9828	9884		1114	2295	3665	4213	7258	9041	9150	4515	4602	5127	5984	5984

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	Top Hit Descriptor	V.alginolyticus sucrase (scrB) gene, complete cds	V.alginolyticus sucrase (scrB) gene, complete cds	zi25b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'	zi25b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds	N.tabacum NelF-4A13 mRNA	Gallus gallus gene for melanocortin 2-receptor, complete cds	Fowlpox virus, complete genome	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6/A-l allele, complete cds	602035589F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183222 5'	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein,	JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,	complete cds; and L-type calcium channel a>	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein,	JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,	complete cds; and L-type calcium channel a>	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds	602118381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5	Rattus norvegicus cytocentrin mRNA, complete cds	Aeropyrum pernix genomic DNA, section 6/7	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha	isoform(RyR1), complete cds	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16	Mus musculus otogelin (Otog), mRNA	Mus musculus otogelin (Otog), mRNA	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5	Drosophila melanogaster 6-pyruvoyltetrahydropterin synthase (pr) gene, complete cds	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'	zu06h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:7311093'	Homo sapiens mRNA for KIAA0614 protein, partial cds	Homo saplens mRNA for KIAA0614 protein, partial cds
	Top Hit Dafabase Source		TN.	EST_HUMAN 2	T_HUMAN		٦	Ę	TN	Ę	T_HUMAN		_		NT				F	EST_HUMAN (INT IN	NT IN			TN.			HUMAN	T_HUMAN			T_HUMAN		TN
,	Top Hit Acession No.	M26511.1	M26511.1	4A678019.1	4A678019.1	29281.1	X79140.1	AB009605.1	AF198100.1	△F065606.1	3F338350.1	J90314.1			4F196779.1				AF236061.1	3F670061.1		AP000063.1			AJ270777.1	7305360 NT	7305360 NT	3F681034.1	3F681034.1		3E904405.1	\A421492.1		AB014514.1
	Most Similar (Top) Hit BLAST E Value	7.3E-01	=	7.3E-01	_	7.2E-01		7.2是-01/	7.2E-01	7.2E-01	7.2E-01	_			7.2E-01			7.2E-01	7.2E-01	7.2E-01	1	_		~ ı	7.1E-01	7.1E-01	7.1E-01	_	7.1E-01	_	7.1E-01	7.1E-01	7.0E-01/	7.0E-01
	Expression Signal	7.42	7.42	3.29	3.29	2.54	3.68	1.46	1.16	2.14	1.31	2.41			1.16			1.16	1.21	2.22	4.78	4.08		10.38	10.8	2.93	2.93	1.56	1.56	6.97	2.25	1.61	1.04	1.04
	ORF SEQ ID NO:	26480	26481	28870			21687	22186	22748	23124	23494	24335			24706			24707	26994	28011	28256			20431	22745	23793	23794	22922	25626	26162	27746		20966	ĺ
	SEQ ID NO:	16315	16315	18585	18585	·10742	11809	12289	12956	13323	13707	14546			14934			14934	16801	17772	18009	19160		10610	12952	14014	14014	15538	15538	16022	17519	19550	11118	11118
	Probe SEQ ID NO:	6454	6454	8729	8729	814	1914	2412	3028	3406	3795	4660			5064			2064	6923	7922	8121	9220		677	3024	4114	4114	5623	5623	6149	7669	9363	1209	1209

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tor	iens cDNA clone IMAGE:288708 3¹ similar to	iens cDNA clone IMAGE:288708 3' similar to		olete genome			elete cds and translational regulator gene, partial	ylete cds and translational regulator gene, partial		IAGE:1085176 3'	Ð	n variable region, isolate PC 2811	١, 69	، 69			ROTEIN FKHL14) (MESENCHYME FORK FACTOR FKH-14)		52-3573470	s cDNA clone IMAGE:1402256 3' similar to PI CHAIN (HUMAN);				1-4	1-4	S	S	IA) (eIF-4C) mRNA, complete cds
Top Hit Descriptor	yz73e07.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;	yz73e07.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;	Homo sapiens chromosome 21 segment HS21C101	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome	AV763842 MDS Homo sapiens cDNA clone MDSCHE04 5'	AV763842 MDS Homo sapiens cDNA clone MDSCHE04 5	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial	cds	nn28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3	Chlamydia muridarum, section 3 of 85 of the complete genome	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69	Homo sapiens DAN gene, complete cds	Homo sapiens DAN gene, complete cds	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENGHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKH-14)	Giardia intestinalis carbamate kinase gene, complete cds	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470	aj75a05.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X56411_ma1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);	Rat(hooded) prolactin gene : exon iii and flanks	Homo sapiens hevin (HEVIN) mRNA	Homo sapiens mRNA for KIAA1345 protein, partial cds	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4	Mus musculus zinc finger protein (Peg3) mRNA, complete cds	Mus musculus zinc finger protein (Peg3) mRNA, complete cds	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds
Top Hit Database Source	EST_HUMAN	EST_HUMAN	LN	NT	EST_HUMAN	EST_HUMAN	LN		TN	EST_HUMAN	LN	TN	IN	NT	N	NT	SWISSPROT	LN LN	N	EST_HUMAN	Z	FZ	LN L	NT	TN	NT	TN	LN
Top Hit Acession No.	N62412.1	N62412.1	2	AE000253.1	AV763842.1	AV763842.1	U69674.1		U69674.1	AA593530.1	AE002271.2	Y17373.1	AL161573.2	AL161573.2	D89013.1	D89013.1	Q99958	7.7	D90917.1	AA854475.1	J00762.1	4758521 NT	AB037766.1	AJ276675.1	AJ276675.1	AF038939.1	AF038939.1	AF164151.1
Most Similar (Top) Hit BLAST E Value	7.0E-01	7.0E-01	7.0E-01	7.0E-01	7.0E-01	7.0E-01	6.9E-01		6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01	6.9E-01		6.8E-01	6.8E-01	6.8E-01	6.8E-01	6.8E-01	6.8E-01	6.8E-01	6.8E-01	6.8E-01	6.8E-01
Expression Signal	1.4	1.4	1.95	8.1	. 2	2	15.73		15.73	2.21	1.63	0.85	2.73	2.73	3.56	3.56	2.37	1.03	1.16	1.58	1.26	0.83	1.52	2.34	2.34	2.59	2.59	1.79
ORF SEQ ID NO:	22173	22174	L		28599		20725				22911	23117	26726		28719	28720		20713		21362		24420	27622	28566	28567	28593	28594	28757
Exon SEQ ID NO:	12277	12277	_	16759	18336	18336	10878		10878	11196	13107	13316	16532		18450	18450	19543	10866	12506	11502	14363	L	17407	18311	18311	18331	18331	18485
Probe SEQ ID NO:	2399	2399	4989	0880	8463	8463	954		954	1288	3182	3339	6652	6652	8582	8582	9016	941	2639	2799	4469	4749	7556	8437	8437	8458	8458	8619

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Top Hit Descriptor	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete ods	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds	zx12g12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element ;	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase	xa95g12x1 NCi_CGAP_Co17 Homo sapiens cDNA clone IMAGE:25745983'	Dendrobium fimbriatum mRNA for phosphoenolpyruvate carboxylase, partial	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome	Gallid herpesvirus 2, complete genome	Gallid herpesvirus 2, complete genome	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GP11	Homo sapiens SLIT1 protein (SLIL2) mRNA, partial cds	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA	C.albicans random DNA marker, 282bp	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis	(HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds	Mus musculus kinesin light chain 2 (Klc2), mRNA	AV660506 GLC Homo sapiens cDNA clone GLCGID04 3'	Homo sapiens chromosome 21 segment HS21C078	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
Top Hit Database Source	Į	IN	EST_HUMAN	LN	N	NT	EST_HUMAN	NT	NT	NT	TN	NT	TN	EST_HUMAN	SWISSPROT	NT	TN	TN	N		NT		EST_HUMAN	NT	NT	NT	片
Top Hit Acession No.	AF213884.1	6.7E-01 AF213884.1	4A451864.1	6.7E-01 AF186073.1	FE 6678580 NT	6.7E-01 X74421.1	6.7E-01 AW079110.1	6.7E-01 AJ252942.1	6.7E-01 AE001486.1	9635035 NT	9635035 NT	6.7E-01 AE004606.1	6.7E-01 AE001486.1	6.7E-01 BF354649.1	014357	6.6E-01 AF075240.1	6.6E-01 AF199339.1	4506880 NT	Y07669.1		6.6E-01 U91328.1	6680577 NT	4V660506.1	6.6E-01 AL163278.2	6.6E-01 AE004382.1	6.5E-01 M75140.1	M75140.1
Most Similar (Top) Hit BLAST E Value	6.7E-01 AF	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01	6.7E-01 014357	6.6E-01	6.6E-01	6.6E-01	6.6E-01 Y0		6.6E-01	6.6E-01	6.6E-01 AV	6.6E-01	6.6E-01	6.5E-01	6.5E-01
Expression Signal	29.34	19.53	1.57	3.59	3.7	96.0	0.85	68.0	1.62	1.42	1.42	3.98	1.46	2.23	3.69	78.0	1.29	1.04	3.05		0.87	3.96	3.63	2.41	1.35	1.37	1.37
ORF SEQ ID NO:	20080		21887	21908	22692		24538										22422	23168				25840			25256	20352	20353
Exon SEQ ID NO:	10259	10295	11989	12713	12893	14246	14762	15046	15542	15723	15723	16192		18200	17903	12329	12532	13362	13522								10544
Probe SEQ ID NO:	295	336	2100	2120	2966	4350	4881	5182	5627	5817	5817	6328	6342	8323	8754	242	2667	3445	3608		4020	5822	6525	7571	9619	809	808

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oligie Exuli Plopes Explessed III neari	Top Hit Descriptor	Mus musculus gene for Tob2, complete cds	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds	Acetobacter xylinum putative ATP binding protein delta-AceB gene, partial cds, and GDP-mannose:cellobiosyl diphosphopolyprenol alpha-mannosyltransferse gene, complete cds	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds	yw17f06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:252515 5'	no15c07.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds	hv74a10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'	S.cerevisiae chromosome IV reading frame ORF YDL097c	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds	Homo sapiens mRNA for KIAA1607 protein, partial cds	M.musculus whn gene	M.musculus whn gene	Treponema pallidum section 63 of 87 of the complete genome	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291126 5'	AV759212 MDS Homo sapiens cDNA clone MDSCGC09 5'	Rat cytomegalovirus Maastricht, complete genome	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)	Haemophilus influenzae Rd section 4 of 163 of the complete genome	nigella flexneri multi-antibiotic resistance locus	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds	Lycopersicon esculentum p69a gene, complete CDS
ie Exori Probe	Top Hit Database Source				NT	MT		LN	TN		EST_HUMAN no		PI DIE	EST_HUMAN h	NT S	OT TN		H L	NT			NT				ISSPROT					NT L
Sirio	Top Hit Acession No.	AB041225.1	4504632 NT	4,127,2265.1	4L161539.2	128921.1	J37258.1		4F119676.1	187583.1	4A601287.1	4U138078.1	AF014115.1	3E465050.1	274145.1			4B046827.1	Y12488.1				BF670405.1	4V759212.1	9845300		U32689.1		-4		Y17275.1
	Most Similar (Top) Hit BLAST E Value	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6.4E-01	6.4E-01	6.4E-01	6.4E-01	6.4E-01	6.4E-01		6.4E-01	6.4E-01		6.3E-01			6.3E-01		6.3E-01
	Expression Signal	5.1	1.08	4.17	98'0	2.27	0.88	1.38	2	3.24	4.03	4.27	2.3	2.79	1.69	5.4	2.45	1.34	0.84	0.84	1.76	13.62	1.44	6.34	1.65	4.41	2.15	3.87	3.89	3.89	0.93
	ORF SEQ ID NO:	23104	23633	23860	23890	24632		26071	28008	28168	28215		28981			20035	23128	23484	24066	24067	27076	27895	27908			20196	20277	21903	22300	22301	
	Exon SEQ ID NO:	13304		14085	14113	14869	15041	15939	17769	17922	17964	18058	18689	19069	19490	10218	13327	13697	14285	14285	16884	17657	17668	19135	19553	10372	10466	12005	12408	Ų	12911
	Probe SEQ ID NO:	3386	3951	4185	4215	4994	5175	6036	7919	8030	8073	8170	8877	9419	9651	252	3410	3785	4389	4389	. 7007	7807	7818	9528	9951	427	524	2116	2534	2534	2983

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	Top Hit Descriptor	D.melanogaster mRNA for metabotropic glutamate receptor	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'	glycoprotein Illa (Alu 1 and 3 fusion junction) [fluman, Genomic Mutant, 300 nt]	Variola virus, complete genome	Variola virus, complete genome	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome	nr09h06.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 O02916 HLARK:	CM-BT043-090299-046 BT043 Homo sapiens cDNA	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION	HYPOTHETICAL 15,3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds	C.limicola pscD gene	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds	ys01e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3'	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds	Rattus norvegicus dihydroxypolyprenylbenzoate methytransferase mRNA, complete cds	Rat TRPM-2 gene, complete cds	Rat TRPM-2 gene, complete cds	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
-	Top Hit Database Source	NT	EST_HUMAN 6				NT	EST HUMAN	T	SWISSPROT	SWISSPROT		ıl IN	NT	ISSPROT	N TN	EST_HUMAN y	EST_HUMAN 6		₽	SWISSPROT F	SWISSPROT F		F	F F	NT						NT IN
	Top Hit Acession No.	99675.1	BE902044.1	S62927.1	9627521 NT	9627521 NT	AE000313.1	AA877715.1		P47003	P36073	9910293 NT	AF105227.1	X83528.1		AF022253.1	H72255.1	E562687:1	124461.1	AL161511.2	P27410	P27410	6678076 NT	20427.1			M64733.1	AF033535.1	11431065 NT	11431065 NT		6.1E-01 AF236117.1
	Most Similar (Top) Hit BLAST E Value	6.3E-01	6.3E-01	6.3E-01	6.3E-01	6.3E-01	6.3E-01	6.3E-01	6.3E-01	6.3E-01	6.3E-01	6.3E-01	6.3E-01	6.3E-01	6.2E-01	6.2E-01	6.2E-01	6.2E-01 B	6.2E-01	6.2E-01	6.2E-01	6.2E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	. 6.1E-01	6.1E-01	6.1E-01
	Expression Signal	1.38	3.17	1.67	2.72	2.72	1.4	2.27	11.72	1.94	1.98	9.21	1.54	1.58	2.12	3.06	5.45	1.71	2.56	7.14	5.02	5.02	4.5	66.0	66.0	3.78	3.78	3.72	1.75	1.75	19.47	19.47
	ORF SEQ ID NO:	23668		27223	27495			28543	<u> </u>	28865	28969	24899			25569		26903			27886	28099	28100				26134	26135	26863		27176		27493
	Exon SEQ ID NO:	13892	_	17027	17288			18288			18680	19697	18944	19619		16287	16710	16448	17336	17649	17857	17857	12225	14809	L.,	15998	15998		16985	16985	17286	17286
	Probe SEQ ID NO:	3985	6929	7150	7421	7421	8004	8413	8647	8725	8868	9128	9220	9435	2278	6426	6831	7435	7476	7799	8007	8007	2345	4931	4931	6104	6104	6792	7108	7108	7419	7419

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Top Hit Descriptor	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71	D(2) DOPAMINE RECEPTOR	UI-H-BI1-aeb-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	SEGMENTATION PROTEIN FUSHI TARAZU	SEGMENTATION PROTEIN FUSHI TARAZU	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)	Gallus gallus mRNA for Hyperion protein, 419 kD isoform	Gallus gallus mRNA for Hyperion protein, 419 kD isoform	#08f07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2095621 3'	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA	Haemophilus influenzae Rd section 16 of 163 of the complete genome	Homo sapiens chromosome 21 segment HS21C067	Homo sapiens chromosome 21 segment HS21C067	Rattus norvegicus cenexin 2 mRNA, partial cds	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds	THYMIDYLATE KINASE (DTMP KINASE)	PM1-DT0041-190100-002-h03 DT0041 Homo sapiens cDNA	Mus spretus strain SPRET/Ei CD48 antigen (Cd48) gene, partial cds	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region	Aspergillus oryzae pyrG gene for orotidine-5-phosphate decarboxylase, complete cds	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]	SIM1 PROTEIN
Top Hit Database Source	NT	NT	E	NT	TN	SWISSPROT	EST_HUMAN	F	ΕŽ	SWISSPROT	SWISSPROT	뉟	SWISSPROT	TN	NT	EST_HUMAN	NT	TN	EST_HUMAN	N	NT	NT	NT	뉟	SWISSPROT	EST_HUMAN	NT	NT	NT	SWISSPROT	SWISSPROT
Top Hit Acession No.	AF119117.1	D87675.1	5802999 NT	AF065253.1	6.0E-01 AJ233396.1	P20288	6.0E-01 AW139713.1	U38813.1	6.0E-01 AJ277661.1	P02835	P02835	6.0E-01 AB008193.1	Q01497	6.0E-01 AJ131892.1	6.0E-01 AJ131892.1	A142062	11421663 NT	9055303 NT		U32701.1	5.9E-01 AL163267.2	5.9E-01 AL163267.2	5.9E-01 AF162756.1	AF065440.2	Q9X0I3	AW937175.1	AF064626.1	1.42320.1		P34926	P40472
Most Similar (Top) Hit BLAST E Value	6.1E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01 P02835	6.0E-01	6.0E-01 Q01497	6.0E-01	6.0E-01		6.0E-01	6.0E-01	6.0E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.8E-01
Expression Signal	1.59	0.92	2.64	1.76	1.02	1.56	2.58	2.61	6.2	4.19	4.19	1.69	1.43	1.78	1.78	2.74	1.64	2.1	2.18	1.25	4.85	4.85	4.12	2.1	2.67	3.1	2.36	1.91	2.18	4.15	1.44
ORF SEQ ID NO:	27860			21103	23438		25086	25968			26795	27727		28541	28542	28939								25917		28454	28669	25342			21637
Exon SEQ ID NO:	17628	10429	10490	11245			15260	15845	ı	16605	16605	17503	17744	18286	18286	18651	19115	19554				13156	14029	15795			18401	18908	l		11763
Probe SEQ ID NO:	7778	486	549	1339	3744	5227	5339	5940	6350	6725	6725	7653	7894	8411	8411	8838	9200	9787	9809	984	3232	3232	4129	5889	8061	8328	8529	9165	9404	9614	1867

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Top Hit Descriptor	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]	Homo sapiens superkiller viralicidic activity 2 (S. cerevistae homolog)-like (SKIVZL), mRNA	Г	Rabbit oral papillomavirus, complete genome	FOS-RELATED ANTIGEN-1	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes,	בייוולם ביים מוחים מחולים מולים מחולים מחולים מתולים מולים מולי	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA	Chlamydophila pneumoniae AR39, section 74 of 94 of the complete genome	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'	NITRATE REDUCTASE [NADPH] (NR)	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)	/wl37g04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-	hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B	(Bf), and complement component C2 (C2) genes,>	Brassica cleracea var. capitata phospholipase D2 (PLD2) gene, complete cds	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds
Top Hit Database Source	LN	SWISSPROT	SWISSPROT	Z	EST_HUMAN	N	SWISSPROT	TN	TN	<u>F</u>	2	ĸ	EST_HUMAN	NT	NT	EST_HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	EST HUMAN			TN	NT	TN	TN	NT	NT
Top Hit Acessian No.	8393912 NT	5.5E-01 P03341	P03341		H46219.1	5.5E-01 AF227240.1	P48755	7657266 NT	T657266	A E02000 8 4	AL 232000.1	AF232006.1	5.4E-01 AW896087.1	5.4E-01 AE002247.2	5.4E-01 AJ276682.1	BF572536.1	5.4E-01 P36858	5.4E-01 Q60675	5.4E-01 Q60675	AI858398.1			5.3E-01 AF019413.1	5.3E-01 AF113919.1	AF113919.1	4506328 NT		AF087658.1
Most Similar (Top) Hit BLAST E Value	5.5E-01	5.5E-01	5.5E-01 P	5.5E-01	5.5E-01	5.5E-01	5.5E-01	5.4E-01	5.4E-01	7 7 2	0.45-01	5.4E-01 A	5.4E-01	5.4E-01	5.4E-01	5.4E-01 BF	5.4E-01	5.4E-01	5.4E-01	5.4E-01 AI			5.3E-01	5.3E-01	5.3E-01 A	5.3E-01	5.3E-01	5.3E-01 A
Expression Signal	1.09	2.88	2 88	1.34	1.39	3.1	1.29	3.74	3.74	Ç	10.7	2.61	2.24	2.78	2.23	2.01	2.87	4.51	4.51	2.12			2.02	0.91	0.91	8.24	8.24	2.92
ORF SEQ ID NO:	20949	22423	22424	ı		22926	23335	19933	19934	2004	20310	20317	21006		21998		28557	28996	28997				20260	21877	21878	22508	22509	22931
Exon SEQ ID NO:	11103	12533	12533		١.	13121	13548	10113	10113	10500	ancol .	10509	11157	11949	12095	17588	18301	18702	18702	18862			10447	11982	11982	12617	12617	13129
Probe SEQ ID NO:	1193	2668	2668	2888	3027	3196	3634	139	139	270	0/6	570	1250	2059	2208	7738	8427	8892	8892	2806			502	2093	2093	2755	2725	3205

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Oligio Evoli i codo Expressod III realt	ORF SEQ Expression (Top) Hit Acession (Top) Hit Acession Signal No. Source Source	1.29 5.3E-01 U39687.1 NT Mycoplasma genitalium section 9 of 51 of the complete genome	25098 1.75 5.3E-01 A1820921.1 EST_HUMAN Zu42h12.95 Soares ovary tumor NbHOT Homo saplens cDNA clone IMAGE:740711 5'	1.75	25447 1.91 5.3E-01 BE645620.1 EST_HUMAN PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);	1.91 5.3E-01 BE645620.1	İ	1.1 EST HUMAN	2.46 5.3E-01 AA916053.1 EST_HUMAN		20904 7.69 5.2E-01 Q9WV30 SWISSPROT (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5) (NF-AT5)	20930 2.83 5.2E-01 AF224492.1 NT Homo sapiens phospholipid scramblase 1 gene, complete cds	5.04 5.2E-01 AL163285.2 NT Homo sapiens chromosome 21 segment HS21C085	2.75 5.2E-01 AB018283.2 NT	TN	1.22 5.2E-01 D73443.1 NT Azotobacter vinelandii iod gene for isocitrate dehydrogenase, complete cds	1.76 5.2E-01 AL116780.1 NT Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	23114 1.9 5.2E-01 AA984165.1 EST_HUMAN am77g05.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504.3'	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A3 (MAGEA3), caltractin	23287 1.06 5.2E-01 U82671.2 NT (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and Ll>	6444 NT	1.28 5.2E-01 AF143952.2 NT	25221 2.46 5.2E-01 AW137066.1 EST_HUMAN UI-H-BI1-acp-a-08-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714799 3'	3.43 6.2E-01 P18516 SWISSPROT DELTA) (RAR-GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-	1.89 5.1E-01 M58509.1	3.28
		1.					c						5.			1.	1.		\ .	_		1.			8		20381 3.
	Exon SEQ ID NO:	14017	15270	15270	15387		17038		1	10728	11061	11086	11739	11988	13008	13124	13278	13314	13494		13496	14826	17611	19260	19370	1	10569
	Probe SEQ ID NO:	4117	5350	5350	5467	5467	7.0	8846	9015	799	1148	1174	1843	2099	3081	3199	3329	3397	3580		3582	4949	7761	9719	9887	601	632

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Table 4
Single Exon Probes Expressed in Heart

Single Laures Lapressed in real	Top Hit Top Hit Descriptor Source	1 NT Polyangium vitellinum (strain PI vt1) 16S rRNA gene	NT R.norvegicus mRNA for mammalian fusca protein	EST_HUMAN	1 EST_HUMAN wi39b12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2427263 3'	SWISSPROT TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)	EST_HUMAN yi94a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872.3'		EST_HUMAN	.1 EST_HUMAN 601556863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'	nac51f10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element EST_HUMAN TAR1 repetitive element;	5552 NT	F	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating	protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes,		Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating brotein (dnaA). ATP operon (atoCDGAHFEB), and butative chromosome replication protein (didA) genes.	뉟	F		NT Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds	.1 EST_HUMAN 601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'		SWISSPROT (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE	SWISSPROT (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]		TN		INT	SWISSPROT NUCLEAR ENVELOPE PROTEIN CUT11
Apressed III lean		angium vitellinum (strain PI vt1) 16S rRi	rvegicus mRNA for mammalian fusca p	39319F1 NIH_MGC_46 Homo sapiens	b12.x1 NCI_CGAP_Ut1 Homo sapiens	NSCRIPTION-REPAIR COUPLING F.	109.s1 Soares placenta Nb2HP Homo	an regenerating protein (reg) gene, con	Human retina cDNA Tsp509I-cleaved	56863F1 NIH_MGC_58 Homo sapiens	iff10.x1 NCI_CGAP_Brn23 Homo sapi 1 repetitive element;	o sapiens postmeiotic segregation incre	o sapiens postmeiotic segregation incre	nera aphidicola genomic fragment con	sin (dnaA), ATP operon (atpCDGAHFE blete cds: and fermination factor Rho (ri	and commenced and commenced traces are	nera aphidicola genomic fragment con in (dnaA), ATP operon (atoCDGAHFE)	olete cds; and termination factor Rho (rl	musculus anti-DNA immunoglobulin lig	o sapiens mRNA for KIAA1184 protein	pus laevis smooth muscle beta-tropom	103871F1 NIH_MGC_19 Homo sapiens	COGEN DEBRANCHING ENZYME (C CANOTRANSFERASE (OLIGO-1,4-1,	(TRIN 6-ALPHA-D-GLUCOSIDASE)]	COGEN DEBRANCHING ENZYME (C CANOTRANSFERASE (OLIGO-1,4-1,	(TRIN 6-ALPHA-D-GLUCOSIDASE)]	45024F1 NIH_MGC_65 Homo sapient	ias latipes gene for membrane guanyly	musculus MRC OX-2 antigen homolog	o sapiens chromosome 21 segment HS	LEAR ENVELOPE PROTEIN CUT11
VOIL FIGURES L	Top Hit atabase	Poly	R.no	Г	Г	Ι.		Г	Г				Hom	Buck	prote		Buch	Сош	Mus	Hom	Xenc				פרת		П	Oryz	Mus	П	
igie L		눌	TN	EST	EST	SMS	EST	둗	EST	EST	EST		2 N	_	F	=		눌	토	Σ	뉟	EST		SWIS		SWIS	EST	Ϋ́	١	F	SIMS
วิ	Top Hit Acession No.	5.1E-01 AJ233944.1	X87885.1	5.1E-01 BF683095.1	5.1E-01 AI858495.1	P96380	5.1E-01 R80873.1	5.1E-01 J05412.1	5.1E-01 W22302.1	5.1E-01 BF030207.1	5.1E-01 BF439982.1	488555	488555		7 OF OB OB 10 4	M 000210.1		AF008210.1	U55574.1	AB033010.1	5.0E-01 M92304.1	5.0E-01 BF317212.1		P35573		P35573	5.0E-01 BE869218.1	5.0E-01 AB021490.2	5.0E-01 AF029215.1	5.0E-01 AL163302.2	013961
	Most Similar (Top) Hit BLAST E Value	5.1E-01	5.1E-01	5.1E-01	5.1E-01	5.1E-01 P96380	5.1E-01	5.1E-01	5.1E-01	5.1E-01	5.1E-01	5.0E-01	5.0E-01		ים מ	0.0		5.0E-01	5.0E-01 U	5.0E-01	5.0E-01	5.0E-01		5.0E-01 P35573		5.0E-01 P35573	5.0E-01	5.0E-01	5.0E-01	5.0E-01	5.0E-01
	Expression Signal	3.28	1.06	1.44	3.84	2.86	1.57	4.54	3.57	3.62	2.03	1.37	1.37		1 30	25.		1.32	0.84	3.44	5.62	3.61		2.25		2.25	1.27	. 9.32	2.26	2.02	2.94
	ORF SEQ ID NO:	20382			23667	23771	26116	27650	27653			21871	21872		24882			21883	23388	23495		26644		27614		27615		29099			
	Exon SEQ ID NO:	10569	11536	11870	13891	13994	15980	17435	17437	19478	19100	11977	11977		11088	1300		11986	13601	13709	16839	16455	-	17401		17401	17791	18806	18913	19349	19358
	Probe SEQ ID NO:	632	1632	1977	3984	4094	6133	7584	7586	9230	9473	2087	2087		2002	7607		2097	3688	3797	6961	7442		7550		7550	7941	9003	9170	9858	6986

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Single Exon Probes Expressed in Heart

	Top Hit Descriptor	602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds	Homo sapiens dlacylglycerol kinase 3 (DAGK3) gene, exon 10	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds	601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds	nq22e11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:11446523'	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products	Saccharomyces cerevisiae) sporulation protein (SPO11) gene required for meiotic recombination, complete		nu85f09.sr1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513	Homo sapiens reproduction 8 (D8S2298E) mRNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4	yi77f10.y5 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element	MER6 repetitive element;	S.cerevisiae ORFs from chromosome X	Trypanosoma cruzi transposon VIP II SIRE repeat region	601584324F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938909 5'	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'	Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds	Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds	RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909198 3'	RC1-ST0278-040400-018-b06 ST0278 Homo sapiens cDNA	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 51	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds	INTERFERON REGULATORY FACTOR 3 (IRF-3)	INTERFERON REGULATORY FACTOR 3 (IRF-3)	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
ייין אייין אייין אייין	Top Hit Database Source	T_HUMAN			N F		T_HUMAN		포 노	EST_HUMAN no		38	NT	EST_HUMAN nu			NT		EST_HUMAN MI		N Tr		EST_HUMAN 60		NT IN	EST_HUMAN R	EST_HUMAN hd	EST_HUMAN R	EST_HUMAN 60	I_HUMAN	NT Bc	SWISSPROT IN	П	EST_HUMAN 60
8 6	Top Hit Acession No.	4.9E-01 BF571462.1	40869.1	-020931.1	4.9E-01 AF020931.1		4.9E-01 BF209791.1	10946863 NT	4.9E-01 AF176912.1	4.9E-01 AA613562.1	4504850 NT			4.8E-01 AA659878.1	5031650 NT	4.8E-01 AL161492.2	4.8E-01 AL161492.2		820744.1	33502.1		4.8E-01 BE790632.1		F102673.1	41069.1	4.7E-01 AW889448.1			4.6E-01 BF693300.1	1.1	4.6E-01 M11267.1			4.6E-01 BE734781.1
	Most Similar (Top) Hit BLAST E Value	4.9E-01	4.9E-01 U	4.9E-01	4.9E-01	4.9E-01	4.9E-01	4.9E-01	4.9E-01	4.9E-01	4.8E-01		4.8E-01	4.8E-01/	4.8E-01	4.8E-01	4.8E-01 /		4.8E-01	4.8E-01 X	4.8E-01	4.8E-01	4.7E-01	4.7E-01	4.7E-01	4.7E-01	4.7E-01	4.6E-01	4.6E-01	4.6E-01	4.6E-01	4.6E-01 Q90643	4.6E-01 Q90643	4.6E-01
	Expression Signal	1.98	1.39	2.46	2.46	1.76	1.41	2.2	1.43	3.55	1.12		8.94	3.94	1.96	3.82	3.82		1.16	2.04	2:52	2.26	8.36	5.77	2.06	2.43	1.36	1.27	1.28	1.28	76.0	3.38	3.38	1.78
	ORF SEQ ID NO:	20541	21634	25688	25689	26429							25153			26601	2992		26679				25953		28564	28853		23375	23383	23384		25111	25112	25372
	Exon SEQ ID NO:		11760	15588	15588	16267	17074	19768	18846	19733	14136		15300	15922	16193	16421	16421		16493	18001	19511	19359	i i	18103	18308	18570	19049	13588	13597	13597	14957	15280	15280	15323
	Probe SEQ ID NO:	772	1864	5679	5679	9049	7197	7359	3065	9851	4577		5381	6018	6330	6563	6563		6613	8111	9369	9870	5925	8221	8434	8682	9330	3674	3683	3683	5087	2360	5360	5404

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Top Hit Descriptor	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:015338 015338 BUTYROPHILIN.;	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:015338 015338 BUTYROPHILIN.;	MEIOSIS SPECIFIC PROTEIN HOP1	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein,	602130953F1 NIH MGC 56 Homo sapiens cDNA clone IMAGE:4287828 5'	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)	L.5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA	L5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA	Human thiopurine methytransferase (TPMT) gene, exon 10 and complete cds	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds	HUM105F03B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-105F03 5'	Linanthus jamauensis maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial ods	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1	zj55d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4541793'	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN	PRECURSOR (HSPG) (PERLECAN) (PLC)	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12	COLLAGEN ALPHA 5(IV) CHAIN	as96e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'	ho60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
Top Hit Database Source	EST_HUMAN	EST_HUMAN	SWISSPROT	TN	ŀ	EST HUMAN	SWISSPROT	SWISSPROT				EST_HUMAN	EST_HUMAN	NT	TN	EST_HUMAN	K	F	N	EST_HUMAN		SWISSPROT	NT	SWISSPROT	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	AI247679.1	AI247679.1	P20050	U62332.1		D62332.1 BF697399.1	P55202	P55202	4.6E-01 AI915634.1	4.6E-01 AI915634.1	P98163	4.6E-01 BE185449.1	BE185449.1	AF019369.1	AF019369.1	D53316.1	4.6E-01 AF120134.1	4.5E-01 AE001931.1	AE001931.1	4.5E-01 AA677086.1		Q05793	4.5E-01 AF126378.1	Q28247	4.5E-01 AI708908.1	4.5E-01 AW873495.1
Most Similar (Top) Hit BLAST E Value	4.6E-01	4.6E-01	4.6E-01	4.6E-01		4.0E-01	4.6E-01	4.6E-01	4.6E-01	4.6E-01	4.6E-01 P98163	4.6E-01	4.6E-01	4.6E-01	4.6E-01	4.6E-01	4.6E-01	4.5E-01	4.5E-01	4.5E-01		4.5E-01 Q05793	4.5E-01	4.5E-01 Q28247	4.5E-01	4.5E-01
Expression Signal	3.29	3.29	1.58	1.47	į	13.48	26.48	26.48	1.33	1.33	2.86	4.78	4.78	5.45	5.45	1.43	2.21	1.73	1.73	4.87		3.97	1.05	1.41	1.1	4.02
ORF SEQ ID NO:	25384	25385	25393			26916			27802	27803		28495		28160	28161			21639	1				23056		23665	
Exon SEQ ID NO:	15334	15334		16040		16722		l				18245	18245		17915	_	19491	11765				- 1	13251		H	15079
Probe SEQ ID NO:	5414	5414	5418	6057		6843	7363	7363	7730	7730	8320	8368	8368	8766	8766	9313	9978	1869	1869	2841		3275	3331	3942	3982	4085

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				!			
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4862	14742	24522	0.94	4.5E-01	BE963445.2	EST_HUMAN	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
5406	15325		1.45	4.5E-01	AW608814.1	EST_HUMAN	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
5983	15888		1.47	4.5E-01	Q00956	SWISSPROT	COAT PROTEIN
6488	16346	26515	2.49	4.5E-01	AI858849.1	EST HUMAN	wi32e02.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923 SWI/SNF COMPLEX 170 KDA SUBUNIT.;
6897	16776			4.5E-01	AI648596.1	EST_HUMAN	tz56g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644.3'
7100	16977		1.54	4.5E-01	11444786 NT	LΝ	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
7991	17841	28082		4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
7991	17841	28083			M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
8237	18117	28369	2.42	4.5E-01	AW591271.1	EST_HUMAN	xo14h01.x1 NCI_CGAP_UB Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6. [1];
9036	19724			4.5E-01	BE871461.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3852961 5'
9694	19245		1.44	4.5E-01	BF337531.1	EST_HUMAN	602035275F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183290 5'
9763	19283		2.15	4.5E-01	11422099 NT	Z	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
9974	19652	24987	1.83	4.5E-01	AF238234.2	NT	Entamoeba histolytica diaphanous protein (dia) gene, partial cds
1991	11885		2.47	4.4E-01	6680503 NT	<u>ا</u>	Mus musculus integral membrane-associated protein 1 (Itmap1), mRNA
		ļ			_		VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
2340	12220			4.4E-01	_	SWISSPROI	IFACI OK)
3274	13195	22994	0.99	4.4E-01	AF058790.1	L	Raftus norvegicus SynGAP-b mRNA, complete cds
3274	13195	22995		4.4E-01	AF058790.1	LN	Rattus norvegicus SynGAP-b mRNA, complete cds
3277	13198		1.87	4.4E-01		EST_HUMAN	7j91d02.y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
4141	14041		1.33	4.4E-01		EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
4924	14803		66.0	4.4E-01	BE141396.1	EST_HUMAN	MR0-HT0078-131299-007-g05 HT0078 Homo sapiens cDNA
5326	15246	25050	1.99	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5326	15246	25051	1.99	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5490	_		1.3	4.4E-01	S65019.1	NT	Imucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5499	15418	25481	1.98	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5'
5624	L	25627	1.6	4.4E-01	AI198413.1	EST HUMAN	qi62h11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' sImilar to TR:Q29168 Q29168 UNKNOWN PROTEIN;
	<u> </u>			100		LI IMANI	qi62h11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 II birknown peottein :
5624	15539	25628	1.6	4.4E-U1	AI198413.1	ESI TOMBIN	DINNOMIN INCIDENT
5782	15688	25798	1.79	4.4E-01	AW080795.1	EST_HUMAN	xc27e08.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE::2585510 3' similar to TR:U95154 U95154 AFLATOXIN B1-ALDEHYDE REDUCTASE.;
6582	16462		10.84	4.4E-01	Z11679.1	NT	S.tuberosum mRNA for induced stolon tip protein (partial)
	ı						

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					,		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7354	17222	27422	1.29	4.4E-01	062836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
7723	17573	27798	1.99	4.4E-01	AI268650.1	EST_HUMAN	qo39f09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
7724	17574		2.45	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
7813	17663	27903	4.67	4.4E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
7935	17785		1.33	4.4E-01	S76404.1	NT	beta -HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
7935	17785		1.33	4.4E-01	S76404.1	NT	beta -HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
9536	18996	25329	2.29	4.4E-01	6677874 NT	TN	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
9306	19663		3.29	4.4E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS210082
9731	19267	25224	5.34	4.4E-01		TN.	Autographa californica nucleopolyhedrovirus, complete genome
9824	19326		1.75	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
405	10351	20178	1.98	4.3E-01	AF155218.1	TN	Callithrix jacchus MW/LW opsin gene, upstream flanking region
405	10351	20179	1.98	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
1585	11489	21350	1.1	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2843	12771		0.96	4.3E-01	AW935269.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3022	12950	22742	0.93	4.3E-01	AW999477.1	EST_HUMAN	MR0-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
3221	13145		1.53	4.3E-01	AE000698.1	NT	Aquifex aeolicus section 30 of 109 of the complete genome
4059	13961	23737	1.15	4.3E-01	J00306.1	NT	Human somatostatin I gene and flanks
4306	10351	20178	1.02	4.3E-01	AF155218:1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4306	10351	20179	1.02	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4875	14755		1.11	4.3E-01	AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
2028	14929		1.06	4.3E-01	_	TN	Xestia c-nigrum granulovirus, complete genome
2600	15514	25592	3.04	4.3E-01	AF179825.1	NT	Saimiri sciureus olfactory receptor (SSC186) gene, partial cds
6028	15933	26064	3.86	4.3E-01	AJ001678.1	TN	Coturnix coturnix japonica ifnG gene
6102	15996		4.01	4.3E-01	033367	SWISSPROT	DNA GYRASE SUBUNIT B
6393	16255		2.54	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158296 5'
6069	16787		2.83	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-I (flaC-flal) genes, complete cds
7608	17459	27674	1.65	4.3E-01	AW630048.1		hh74e10,y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 51
7608	17459	27675	1.65	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
7070	06224	23026	4 07	A 95 04	A1M/470EED 4	TOT LIMANI	xn63e05.x1 Soares_NHCeC_cervical_tumor Homo eapiens cDNA clone IMAGE:2698400 3' similar to
7/0/			1,2,1	1.0-10.4	AF075000.1	וטואוטו ביי	
8302			2.64	4.3⊏-01	AF075629.1	Z	Equus capailus microsatellite LEXUZ/
8537	18409		1.98	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
8537		28674	1.98	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-290200-013-012 BN0034 Homo sapiens cDNA
9916	19390		2.02	4.3E-01	AJ003022.1	님	Streptomyces coelicolor whilh gene

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· Top Hit Descriptor	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR	nz24a09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288696 3'	Xyella fastidiosa, section 93 of 229 of the complete genome	ql94b01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'	QV0-LT0015-180200-127-h01 LT0015 Homo sapiens cDNA	SOX-8 PROTEIN	RC5-BT0559-020300-013-E06 BT0559 Homo sapiens cDNA	nj69h01.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);	yf77e01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28278 5'	601879721F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4108493 5'	RC3-CT0254-060400-029-g04 CT0254 Homo sapiens cDNA	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'	Brca1=breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47	EST369413 MAGE resequences, MAGE Homo sapiens oDNA	EST369413 MAGE resequences, MAGE Homo sapiens cDNA	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA	MR3-SN0010-280300-103-h07 SN0010 Home sapiens cDNA	Oryzias latipes OIGC7 mRNA for membrane guanyly cyclase, complete cds	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:39060853'	AV731815 HTF Homo sapiens cDNA clone HTFBHH05 5'	RC-BT091-210199-142 BT091 Homo sapiens cDNA	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'	PM-BT103-270499-684 BT103 Homo sapiens cDNA	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36	oj94b08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943.3'	Rhodococcus sp. AD45 isoG, isoH, isoI, isoJ, isoA, isoB, isoC, isoD, isoE and isoF genes	
Top Hit Database Source	SWISSPROT	EST_HUMAN n	Г	EST_HUMAN q		SWISSPROT	EST_HUMAN R	EST_HUMAN II	EST_HUMAN M	EST_HUMAN 6	EST_HUMAN R	EST_HUMAN A	T_HUMAN	NT (B	NT N		Г		T HUMAN			EST_HUMAN A	EST_HUMAN R			EST_HUMAN P		NT TN	NT IN	EST_HUMAN o	NT R	
Top Hit Acession No.	Q39102	AA761653.1	AE003947.1	Al280338.1	AW835527.1	Q04886	BE073574.1	AA534093.1	R13467.1	BF242055.1	AW854162.1	AU158472.1	AU158472.1	S82504.1		AW957448.1	AW957448.1	4758039 NT	AW863666.1	AB023489.1	BE966485.2	AV731815.1	Al905481.1	AV705243.1	1	AI905949.1	7705283 NT	AL161536.2	AL161536.2		AJ249207.1	
Most Similar (Top) Hit BLAST E Value	4.2E-01	4.2E-01	4.2E-01	4.2E-01		4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01			_	4.2E-01	4.2E-01	4.2E-01	4.2E-01	_				4.1E-01	4.1E-01	_	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	4.1E-01	
Expression Signal	1.04	0.89	4.78	1.09	0.96	-	3.63	4.96	3.13	1.5	1.56	9.1	9.1	2.1	5.91	2.1	2.1	1.19	1.48	2.2	2.04	1.66	1.88	2.4	2.4	1.03	1.52	1.76	1.76	1.13	2.59	
ORF SEQ ID NO:	21099		23263	23288	23503	23595		24273	24350	25484	25518	26164	26165	26219	26233	26739	26740	26844	28084	28528	28799		20835	20844	20845	21356	22434	22633	22634	22985	23852	-
Exon SEQ ID NO:	12691	11800	13472	13499	13715	13810	14438	14487	14557	15422	15450	16024	16024	19461	16083	16543	16543	16655	17842	18276	18517	19353	10994	11003	11003	11496	12543	12836	12836	13186	14077	
Probe SEQ ID NO:	1335	1904	3558	3585	3803	3900	4545	4599	4671	5503	5533	6151	6151	6184	6217	6999	6999	9229	7992	8400	8699	8863	1078	1087	1087	1592	2678	2910	2910	3263	4177	

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Table 4
Single Exon Probes Expressed in Heart

SEQ Expression (Top) Hit Top Hit Acession No. Signal BLASTE No. Source	ye43h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains 4.11 3.8E-01 T95413.1 EST_HUMAN Alu repetitive element, contains PTR5 repetitive element;		2.57 3.8E-01 R42550.1 EST_HUMAN	2.57 3.8E-01 R42550.1 EST_HUMAN	2.38 3.8E-01 AE001124.1 NT Borrella burgdorferl (section 10 of 70) of the complete genome	1.34 3.8E-01 U94788.1 NT Human p53 (TP53) gene, complete cds			1.37 3.8E-01 T54787.1		1.33	9.85 3.7E-01 AB037831.1	9.48	6.63		3.32	2.73 3.7E-01 11525843 NT	4.51 3.7E-01 BE873743.1 EST_HUMAN			2.34 3.7E-01 11436739 NT	1.46 3.7E-01 AJ271386.1 NT	3.93 3.7E-01 AI336411.1 EST_HUMAN	28365 1.81 3.7E-01 X05958.1 NT Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)	2.66 3.7E-01	2.66 3.7E-01 AJ297357.1	4.23 3.7E-01 X04122.1	2.76 3.7E-01 6677678 NT Mus musculus retinoblastoma 1 (Rb1), mRNA	1.87 3.7E-01 J04982.1 NT Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds	3.7E-01 AJ243525.1 NT	2.41 3.7E-01 D86976.1 NT Human mRNA for KIAA0223 gene, partial cds
	4.11	2.82			2.38	1.34	2.21	1.84																				2.76	1.87	1.94	2.41
ORF SEQ	40	33		47 29042	16	191	37	38		06 25180										27 26921				13 28365			111 28155	84	03	17	176
e Exon ID SEQ ID NO:	16 17304	20 18633		39 18747	97 18997	22 19661	30 19137	17 19638	21 19675		70 19430	31 12308	1	36 14036	25 14123	92 14190								32 18113		92 18268	62 17911	79 18784	19303		72 18976
Probe SEQ ID NO:	7516	8820	89.	8939	9297	9422	9530	9917	66	9937	9970	2431	3414	4136	4225	4292	623	638	6392	789	6848	73(7864	8232	8392	83	8762	8979	8006	91.	9272

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9634	19206		2.18	3.7E-01	AL121154.1	EST_HUMAN	DKFZp762K075_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5'
9701	19251	25217	1.52	3.7E-01	Y18000.1	TN	Homo sapiens NF2 gene
9964	19746		1.31	3.7E-01	AJ237934.1	TN	Bos taurus partial stat5B gene, exons 2-15 and joined CDS
626	10902		7.17	3.6E-01	U89241.1	ᅜ	Human mibp gene, partial cds
1292	11199	21054	2.59	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Scares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1292		21055	2.59	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1874	11770	21645	6.05	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1874	11770	21646	6.05	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1908	11803	21682	6.18	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2007	11899		1.08	3.6E-01	AF056927.1	TN	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2223	12108		1.04	3.6E-01	AB002321.1	TN	Human mRNA for KIAA0323 gene, partial cds
2341	12221		2.39	3.6E-01	X76725.1	N	P. irregulare (P3804) gene for actin
2437	12314	22211	1.63	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
							PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE
							METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-
2589	12460	22350	2.28		P24206	SWISSPROT	ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2869	15077		8.9		AF199485.1	덛	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
3424	13341	23145	1.85	3.6E-01	X76758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
3424	13341	23146	1.85	3.6E-01	X76758.1	TN	H.sapiens serotonin transporter gene, exons 9 and 10
4308	14205	23988	1.16	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4635	14523	24312	0.85	3.6E-01	AJ009609.1	TN	Brassica napus mRNA for MAP4K alpha2 protein
4684	14570	24367	1.23		AJ229237.1	ᅜ	Bacteria from anoxic bulk soil 16S rRNA gene (strain XB45)
4941	14819	24587	2.01		AW339393.1	EST_HUMAN	ha02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5899	15805	25928	1.6	3.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
6238	16104		5.49	3.6E-01	R94090.1	EST_HUMAN	yt74a06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:275987 5'
	1						wt72c10.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
6317	-)	26340	1.66	١	AW027174.1	EST HUMAN	O15117 FYN BINDING PROTEIN. [1];
6816	16695	26886	13.42	3.6E-01	AL161583.2	F	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
7205	17082	27269	3.37	3.6E-01	4504956 NT	<u>I</u>	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7205	J	07.67.6	3.37	3.6F-01	4504056 NT	L	Homo sapiens Ivsosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7302	1_	27380	14	3.6F-01	AI 163204 2	Ę	Homo sapiens chromosome 21 segment HS21C004
7677	1	27750	78.47		053404	TORDEOT	PROBABI F PEPTIDE ARC TRANSPORTER ATP-RINDING PROTEIN Y4TS
100	J	OC / /7	10.04	١	K00 194	٦	

WO 01/57274 PCT/US01/00666

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Purple Exm Purp								
18191 28440 1.94 3.6E-01 BE502390.1 EST_HUMAN 1826 28686 3.69 3.6E-01 AE004293.1 NT 17850 28134 3.69 3.6E-01 AE000856.1 NT 18761 1.81 3.6E-01 AF000335.1 NT 1886 3.05 3.6E-01 AF000335.1 NT 1886 3.05 3.6E-01 AF000335.1 NT 19704 3.05 3.6E-01 AV190229.1 EST_HUMAN 10596 20414 0.97 3.5E-01 AL161581.2 NT 10640 20467 1.24 3.5E-01 AL161581.2 NT 10640 20467 1.24 3.5E-01 AL161581.2 NT 11664 20467 1.24 3.5E-01 AL161881.2 NT 11664 20467 1.24 3.5E-01 AL161881.2 NT 11664 20531 1.17 3.5E-01 AC123252.1 NT 11668 2	Probe SEQ ID NO:			Expression Signal	Most Similar (Top) Hit BLAST E Value	ssion	Top Hit Database Source	Top Hit Descriptor
1826 28685 3.69 3.6E-01 AB004293.1 NT 17890 28134 3.69 3.6E-01 AE000856.1 NT 18761 1.81 3.6E-01 AE000836.1 NT 18886 3.05 3.6E-01 AF000335.1 NT 18886 3.05 3.6E-01 AV190229.1 EST_HUMAN 19704 1.28 3.6E-01 AV190229.1 EST_HUMAN 10540 20461 0.97 3.5E-01 AL161581.2 NT 10640 20467 1.24 3.5E-01 AL161881.2 NT 10640 20467 1.24 3.5E-01 AL161881.2 NT 10640 20467 1.24 3.5E-01 AL161881.2 NT 11664 20531 3.17 3.5E-01 AF012576.1 NT 11665 21384 1.05 3.5E-01 AC01253.1 NT 14765 22462 1.29 3.5E-01 AF01253.1 NT 14765 2	8314	1					EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
17890 28134 3.56 3.6E-01 AE000856.1 NT 18761 1.81 3.6E-01 AE000356.1 NT 18866 3.05 3.6E-01 AF000335.1 NT 19704 1.83 3.6E-01 AE000335.1 NT 19704 1.58 3.6E-01 AW190229.1 EST_HUMAN 10774 19990 2.18 3.5E-01 AV190229.1 EST_HUMAN 10640 20467 1.24 3.5E-01 AV190229.1 EST_HUMAN 10640 20466 1.24 3.5E-01 AA223252.1 EST_HUMAN 11508 27327 1.85 3.5E-01 BF310688.1 EST_HUMAN 11528 22327 1.85 3.5E-01 BF310688.1 EST_HUMAN 11529 2334 1.05 3.5E-01 BF310688.1 NT 14076 2355-01 BF310688.1 NT NT 14275 2462 0.86 3.5E-01 BF310688.1 NT 14675 <	8453						NT	Arabidopsis thaliana mRNA for SigB, complete cds
17890 28134 3.66 3.6E-01 AE000856.1 NT 1886 3.05 3.6E-01 Y19210.1 NT 1888 3.05 3.6E-01 AV190229.1 EST_HUMAN 19704 1.58 3.6E-01 AV190229.1 EST_HUMAN 10774 19900 2.18 3.6E-01 AV190229.1 EST_HUMAN 10596 2.0444 0.97 3.5E-01 AV190229.1 EST_HUMAN 10640 2.0466 1.24 3.5E-01 AV190229.1 EST_HUMAN 11508 2.0357 1.24 3.5E-01 AV190229.1 EST_HUMAN 11508 2.1370 1.17 3.5E-01 BF310688.1 EST_HUMAN 11508 2.1384 1.05 3.5E-01 BF310688.1 EST_HUMAN 12725 2.2327 1.85 3.5E-01 BF310688.1 EST_HUMAN 14275 2.2462 0.86 3.5E-01 BF146885.1 EST_HUMAN 14730 24462 0.84 3.5E-01 BF1468								Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete
19761 1.81 3.6E-01 Y19210.1 NT 1886 3.05 3.6E-01 AE000335.1 NT 18963 3.05 3.6E-01 AE000335.1 NT 19704 1.58 3.6E-01 AW190229.1 EST_HUMAN 10774 19990 2.18 3.5E-01 AV190229.1 EST_HUMAN 10640 20467 1.24 3.5E-01 AT06188 NT NT 10694 20467 1.24 3.5E-01 AT06188 NT NT 11508 21370 1.17 3.5E-01 BF128796.1 EST_HUMAN 11508 21384 1.05 3.5E-01 BF128796.1 EST_HUMAN 11508 21384 1.05 3.5E-01 BF128796.1 EST_HUMAN 14075 24402 0.86 3.5E-01 BF12876.1 NT 14675 24402 0.84 3.5E-01 BF146886.1 EST_HUMAN 14675 24402 0.84 3.5E-01 BF146886.1 NT <	8741				3.6E-01		NT	genome
1886 3.05 3.6E-01 AE000335.1 NT 18983 3.05 3.6E-01 AE000335.1 NT 19704 1.58 3.6E-01 AV190229.1 EST_HUMAN 10174 19990 2.18 3.6E-01 AV190229.1 EST_HUMAN 10640 20414 0.97 3.5E-01 AT06136 NT 10640 20467 1.24 3.5E-01 AT06136 NT 10694 20467 1.24 3.5E-01 AT06136 NT 11508 21370 1.77 3.5E-01 BF128796.1 EST_HUMAN 11508 21370 1.17 3.5E-01 BF310688.1 EST_HUMAN 11508 21384 1.05 3.5E-01 U05897.1 NT 14065 22327 1.85 3.5E-01 U05897.1 NT 14675 24462 0.84 3.5E-01 U05897.1 NT 14675 24462 0.84 3.5E-01 M1448042 NT 14	9044			1.81			NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
19704 3.03 3.6E-01 U66888.1 NT 19704 1.58 3.6E-01 AW190229.1 EST_HUMAN 10174 19990 2.18 3.6E-01 AV190229.1 EST_HUMAN 10596 2.0414 0.97 3.5E-01 7706136 NT 10640 2.0466 1.24 3.5E-01 7706136 NT 10694 2.0467 1.24 3.5E-01 7706136 NT 10694 2.0467 1.24 3.5E-01 7706136 NT 10694 2.0531 3.17 3.5E-01 BF129796.1 EST_HUMAN 11508 2.1370 1.17 3.5E-01 BF310688.1 EST_HUMAN 14275 2.2327 1.26 3.5E-01 BF146585.1 EST_HUMAN 14275 2.4462 0.84 3.5E-01 BF146585.1 EST_HUMAN 14730 2.4462 0.84 3.5E-01 M182349.1 NT 14730 2.4462 0.84 3.5E-01 M18203.1	9127	L		3.05			NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
19704 1.58 3.6E-01 AW190229.1 EST_HUMAN 10174 19990 2.18 3.6E-01 6678933 NT 10596 20414 0.97 3.5E-01 7706136 NT 10640 20466 1.24 3.5E-01 7706136 NT 10640 20467 1.24 3.5E-01 7706136 NT 10694 20467 1.24 3.5E-01 7706136 NT 11508 21370 1.17 3.5E-01 BF310688.1 EST_HUMAN 11526 21384 1.05 3.5E-01 BF310688.1 EST_HUMAN 14275 22327 1.85 3.5E-01 BF310688.1 EST_HUMAN 14675 2462 0.86 3.5E-01 BF310688.1 BST_HUMAN 14675 2462 0.84 3.5E-01 BF310688.1 NT 14675 2462 0.84 3.5E-01 BF310688.1 NT 14675 2462 0.84 3.5E-01 BF310688.1	9281			3.03	3.6E-01		IN	Mus musculus Emr1 mRNA, complete cds
10174 19990 2.18 3.5E-01 6678933 NT 10596 20414 0.97 3.5E-01 AL161581.2 NT 10640 20466 1.24 3.5E-01 7706136 NT 10640 20467 1.24 3.5E-01 7706136 NT 11508 21370 1.17 3.5E-01 BF310688.1 EST_HUMAN 11526 21384 1.05 3.5E-01 BF310688.1 EST_HUMAN 12725 22327 1.85 3.5E-01 U05897.1 NT 14065 23839 1.92 3.5E-01 AF071253.1 NT 14750 24462 0.86 3.5E-01 AF071253.1 NT 14750 24462 0.84 3.5E-01 AF071253.1 NT 14750 24513 3.84 3.5E-01 AF071253.1 NT 16584 1.8 3.5E-01 AF07430.2 NT 16589 3.2 3.5E-01 AF0760.0 NT	6886	<u> </u>		1.58	3.6E-01	V190229.1	EST_HUMAN	xi60e11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
10596 20414 0.97 3.5E-01 AL161581.2 NT 10640 20466 1.24 3.5E-01 7706136 NT 10640 20467 1.24 3.5E-01 7706136 NT 11508 20531 3.17 3.5E-01 BF310688.1 EST HUMAN 11526 21384 1.05 3.5E-01 BF310688.1 EST HUMAN 12725 22327 1.85 3.5E-01 U35776.1 NT 14076 23839 1.92 3.5E-01 AA223252.1 EST HUMAN 14075 2465 1.29 3.5E-01 AF071253.1 NT 14675 2465 0.84 3.5E-01 AF071253.1 NT 14675 2465 0.84 3.5E-01 AF071253.1 NT 14676 23839 1.92 3.5E-01 AF071253.1 NT 14675 2465 0.84 3.5E-01 AF048042 NT 16584 27238 3.27 3.5E-01 AF0	202	1			3.5E-01		IN	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
10640 20466 1.24 3.5E-01 7706136 NT 10640 20467 1.24 3.5E-01 7706136 NT 10694 20531 3.17 3.5E-01 BF128796.1 EST HUMAN 11508 21370 1.17 3.5E-01 BF310688.1 EST HUMAN 12725 22327 1.85 3.5E-01 U35776.1 NT 14065 23839 1.92 3.5E-01 MA223252.1 EST HUMAN 14075 24056 1.29 3.5E-01 MF071253.1 NT 14675 24652 0.84 3.5E-01 MR349.1 NT 14675 24462 0.84 3.5E-01 MR349.1 NT 14676 23839 3.47 3.5E-01 MR349.1 NT 14675 24462 0.84 3.5E-01 MR349.1 NT 16584 3.5E-01 MR349.1 NT NT 16584 3.5E-01 MR349.1 NT MR <t< td=""><td>662</td><td></td><td></td><td></td><td>3.5E-01</td><td></td><td>NT</td><td>Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77</td></t<>	662				3.5E-01		NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
10640 20467 1.24 3.5E-01 7706136 NT 10694 20531 3.17 3.5E-01 BF129796.1 EST_HUMAN 11508 21370 1.17 3.5E-01 BF310688.1 EST_HUMAN 12525 21384 1.05 3.5E-01 U35776.1 NT 12637 0.86 3.5E-01 U05897.1 NT 14065 23839 1.92 3.5E-01 AF071253.1 NT 14075 24056 1.29 3.5E-01 BE146585.1 EST_HUMAN 14675 24462 0.84 3.5E-01 BE146585.1 EST_HUMAN 15699 1.29 3.5E-01 M18349.1 NT 16584 3.84 3.5E-01 M18349.1 NT 17048 27238 3.21 3.5E-01 A507610 NT 17048 27238 3.21 3.5E-01 A50236 NT 1763 2764 1.51 3.5E-01 A50230 NT 17658 <td>708</td> <td></td> <td>L</td> <td></td> <td>3.5E-01</td> <td></td> <td>NT</td> <td>Homo sapiens GAP-like protein (LOC51306), mRNA</td>	708		L		3.5E-01		NT	Homo sapiens GAP-like protein (LOC51306), mRNA
10694 20531 3.17 3.5E-01 BF129796.1 EST_HUMAN 11508 21370 1.17 3.5E-01 BF310688.1 EST_HUMAN 11526 21384 1.05 3.5E-01 U35776.1 NT 12725 22327 1.85 3.5E-01 U05897.1 NT 14065 23839 1.92 3.5E-01 MF071253.1 NT 14075 2465 1.29 3.5E-01 BE146585.1 EST_HUMAN 14675 2462 0.84 3.5E-01 MR349.1 NT 14675 2462 0.84 3.5E-01 MR349.1 NT 14676 2462 0.84 3.5E-01 MR349.1 NT 16584 3.84 3.5E-01 MR349.1 NT 17048 27238 3.21 3.5E-01 MR349.1 NT 17048 27238 3.21 3.5E-01 MR349.1 NT 17538 27764 5 3.5E-01 MR349.1 NT <td>708</td> <td></td> <td>L</td> <td>1.24</td> <td>3.5E-01</td> <td></td> <td>NT</td> <td>Homo sapiens GAP-like protein (LOC51306), mRNA</td>	708		L	1.24	3.5E-01		NT	Homo sapiens GAP-like protein (LOC51306), mRNA
11508 21370 1.17 3.5E-01 BF310688.1 EST_HUMAN 11526 21384 1.05 3.5E-01 U35776.1 NT 12725 22327 1.85 3.5E-01 U05897.1 NT 14065 23839 1.92 3.5E-01 MF071253.1 NT 14075 24056 1.29 3.5E-01 MF071253.1 NT 14675 24462 0.84 3.5E-01 MB1403.1 NT 14676 24462 0.84 3.5E-01 MR349.1 NT 14676 24462 0.84 3.5E-01 MR349.1 NT 14679 24513 3.84 3.5E-01 MR349.1 NT 16584 1.88 3.5E-01 M8349.1 NT 17048 27768 3.5E-01 M8349.1 NT 17048 27768 3.5E-01 A507610 NT 18005 2851 2.56-01 X61084.1 NT 18006 2851 2.56-01	763				3.5E-01	BF129796.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
11526 21384 1.05 3.5E-01 U35776.1 NT 12725 22327 1.85 3.5E-01 AA223252.1 EST_HUMAN 12537 0.86 3.5E-01 AF071253.1 NT 14065 23839 1.92 3.5E-01 AF071253.1 NT 14675 24462 0.84 3.5E-01 BE146585.1 EST_HUMAN 14675 24462 0.84 3.5E-01 M18203.1 NT 1584 3.84 3.5E-01 M18203.1 NT 1584 3.47 3.5E-01 M18349.1 NT 17048 27238 3.21 3.5E-01 M18349.1 NT 17048 27758 3.21 3.5E-01 M1848042 NT 1765 27680 1.51 3.5E-01 A507610 NT 18005 2851 2.59 3.5E-01 X61084.1 NT 18263 2851 2.34 3.5E-01 X61084.1 NT 18263 <td< td=""><td>1603</td><td></td><td></td><td></td><td>3.5E-01</td><td>BF310688.1</td><td>EST_HUMAN</td><td>601894653F2 NIH MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5</td></td<>	1603				3.5E-01	BF310688.1	EST_HUMAN	601894653F2 NIH MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5
12725 22327 1.85 3.5E-01 AA223252.1 EST_HUMAN 12637 0.86 3.5E-01 U05897.1 NT 14065 23839 1.92 3.5E-01 AF071253.1 NT 14075 24462 0.84 3.5E-01 BE146885.1 EST_HUMAN 14730 24513 3.84 3.5E-01 M81203.1 NT 1584 3.47 3.5E-01 M8349.1 NT 16584 3.47 3.5E-01 X98505.1 NT 17048 27238 3.21 3.5E-01 A507010 NT 1753 27680 1.51 3.5E-01 A507010 NT 1805 2851 2.99 3.5E-01 X61084.1 NT 18263 28513 2.34 3.5E-01 A507010 NT 18263 28514 2.34 3.5E-01 A1243178.1 NT	1622	l					NT	Raftus norvegicus ADP-ribosylation factor-directed GTP ase activating protein mRNA, complete cds
12537 0.86 3.5E-01 (105897.1) NT 14065 23839 1.92 3.5E-01 (105897.1) NT 14275 24056 1.29 3.5E-01 (129)	2563				3.5E-01	AA223252.1	EST_HUMAN	zr08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
14066 23839 1.92 3.5E-01 AF071253.1 NT 14275 24056 1.29 3.5E-01 BE146585.1 EST HUMAN 14730 24513 3.84 3.5E-01 N81203.1 EST HUMAN 15959 3.47 3.5E-01 M18349.1 NT 16584 1.88 3.5E-01 X98605.1 NT 17048 27238 3.21 3.5E-01 4507610 NT 17463 27680 1.51 3.5E-01 4507610 NT 18005 28251 2.99 3.5E-01 X61084.1 NT 18263 28513 2.36 3.5E-01 X61084.1 NT 18263 28514 2.34 3.5E-01 AL243178.1 NT	2672		-	0.86			NT	Fibrobacter succinogenes S85 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds
14275 24056 1.29 3.5E-01 BE146585.1 EST HUMAN 14730 24513 3.84 3.5E-01 IM1203.1 EST HUMAN 15959 3.47 3.5E-01 M18349.1 NT 16584 3.47 3.5E-01 M18349.1 NT 17048 27238 3.21 3.5E-01 M1448042 NT 17048 27238 3.21 3.5E-01 4507610 NT 17463 27680 1.51 3.5E-01 202294 SWISSPROT 18005 28251 2.99 3.5E-01 XG1084.1 NT 18263 28513 2.34 3.5E-01 AL243178.1 NT 18263 28514 2.34 3.5E-01 AL243178.1 NT	4165						NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
14675 24462 0.84 3.5E-01 N81203.1 EST HUMAN 14730 24513 3.84 3.5E-01 M18349.1 NT 16584 3.47 3.5E-01 X98605.1 NT 17048 27238 3.21 3.5E-01 4507610 NT 17463 27680 1.51 3.5E-01 4507610 NT 18005 28251 5 3.5E-01 X61084 SWISSPROT 18263 28513 2.99 3.5E-01 X61084.1 NT 18263 28514 2.34 3.5E-01 AL243178.1 NT	4379						EST_HUMAN	RC5-HT0218-181099-011-g02 HT0218 Homo sapiens cDNA
14730 24513 3.84 3.5E-01 M18349.1 NT 15959 3.47 3.5E-01 X98505.1 NT 17048 27238 3.21 3.5E-01 11448042 NT 17048 27238 3.21 3.5E-01 4507610 NT 17538 27764 5 3.5E-01 Z26825.1 NT 18005 28251 2.99 3.5E-01 X61084.1 NT 18263 28513 2.34 3.5E-01 AJ243178.1 NT 18263 28514 2.34 3.5E-01 AJ243178.1 NT	4790						EST_HUMAN	788iE1 fetal brain cDNA Homo sapiens cDNA clone 788iE1-K similar to R07879, Z40498
15959 3.47 3.5E-01 X98505.1 NT 16584 1.88 3.5E-01 11448042 NT 17048 27238 3.21 3.5E-01 4507610 NT 17463 27764 1.51 3.5E-01 22825.1 NT 17538 27764 5 3.5E-01 Z28825.1 NT 18005 28251 2.99 3.5E-01 X61084.1 NT 18263 28513 2.34 3.5E-01 AJZ43178.1 NT 18263 28514 2.34 3.5E-01 AJZ43178.1 NT	4849		L				NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
16584 1.88 3.5E-01 11448042 NT 17048 27238 3.21 3.5E-01 4507610 NT 17463 27764 1.51 3.5E-01 226825.1 NT 18005 28251 2.99 3.5E-01 X61084.1 NT 18263 28513 2.34 3.5E-01 AJ243178.1 NT 18263 28514 2.34 3.5E-01 AJ243178.1 NT	6199			3.47	3.5€-01	X98505.1	NT	S.scrofa mRNA for CD31 protein (PECAM-1)
17048 27238 3.21 3.5E-01 4507610 NT 17463 27680 1.51 3.5E-01 Q02294 SWISSPROT 17538 27764 5 3.5E-01 Z26825.1 NT 18005 28251 2.99 3.5E-01 X61084.1 NT 18263 28513 2.34 3.5E-01 AJ243178.1 NT 18263 28514 2.34 3.5E-01 AJ243178.1 NT	6704			1.88	3.5E-01		. TN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
17463 27680 1.51 3.5E-01 Q02294 SWISSPROT 17538 27764 5 3.5E-01 Z26925.1 NT 18005 28251 2.99 3.5E-01 XG1084.1 NT 18263 28513 2.34 3.5E-01 AJ243178.1 NT 18263 28514 2.34 3.5E-01 AJ243178.1 NT	7171				3.5E-01		NT	Homo sapiens tyrosine kinase non-receceptor 1 (TNK1), mRNA
17538 27764 5 3.5E-01 Z2825.1 NT 18005 28251 2.99 3.5E-01 X61084.1 NT 18263 28513 2.34 3.5E-01 AJ243178.1 NT 18263 28514 2.34 3.5E-01 AJ243178.1 NT	7612				3.5F-04	002294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-18 SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
18005 28251 2.99 3.5E-01 X61084.1 NT 18263 28513 2.34 3.5E-01 AJ243178.1 NT 18263 28514 2.34 3.5E-01 AJ243178.1 NT	7688	1_			3.5E-01		N	X.laevis gene for albumin including HP1 enhancer
18263 28513 2.34 3.5E-01 AJ243178.1 NT 18263 28514 2.34 3.5E-01 AJ243178.1 NT	8116	i .	ĺ.,				NT	C.griseus rhodopsin gene for opsin protein
18263 28514 2.34 3.5E-01 AJ243178.1 NT	8386	ΙI					NT	Gailus gailus SPARC gene for osteonectin, promoter and exon 1
	8386					1243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1

Page 47 of 413 Table 4 Single Exon Probes Expressed in Heart

. Top Hit Descriptor	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13	B.taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit	ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'	ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line	Pseudomonas fluorescens coIR, coIS genes, orf222 and partial inaA gene	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens chromosome 21 segment HS21C010	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete	cds	7n94a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15 Q9UJ15 DJ18C9.1;	no11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA	hy17d09x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3197585 3' similar to contains L1.t3 L1 repetitive element;	qi95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive	element;	Sea urchin hsp70 gene II for heat shock protein 70	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90	zn12d11.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:547221 3'	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds	UI-H-BI1-aei-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'		zb53e12.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'
Top Hit Database Source	INT	TN	EST_HUMAN	EST_HUMAN	卢	뉟	닏	LN TN	NT	٦	M	TN		۲	EST_HUMAN	EST_HUMAN	뉟	EST_HUMAN	EST HUMAN		EST_HUMAN	N	NT	EST_HUMAN	뇐	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	3.5E-01 AL161501.2	3.5E-01 X64565.1	H80814.1	3.5E-01 H80814.1	AJ242956.1	Y09798.2	Y00554.1	D90909.1	3.4E-01 AL161516.2	3.4E-01 AL163210.2	3.4E-01 AL163210.2	U83905.1		AF106835.1	3.4E-01 BF449010.1	3.4E-01 AA584196.1	3.4E-01 AF166341.1	3.4E-01 BE069912.1	BE463761.1		3.4E-01 AI240973.1	3.4E-01 X16544.1	3.4E-01 AL161594.2	3.4E-01 AA085313.1	L02971.1	AW204505.1	3.4E-01 AL120544.1	N95225.1
Most Similar (Top) Hit BLAST E Value	3.5E-01	3.5E-01	3.5E-01	3.5E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01		3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01		3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01 ₽	3.4E-01	3.4E-01
Expression	3.34	2.12	2.25	2.25	1.9	4.53	1.73	2.81	1.46	0.81	0.81	5.41		3.48	2.33	1.16	0.78	1.82	0.93		3.57	1.2	2.85	4.71	2.06	2.57	1.47	1.52
ORF SEQ ID NO:	29052		24999	25000		20731	21066	22129			22698	22846		23209			24074	24221	. 24494				25469				25796	
Exon SEQ ID NO:	Ιİ	18937	19616	19616	10624	10883					12898	13049		13404	13634	13872	14290	14437	14710	l	14750	14845	15406	15467	15566			15948
Probe SEQ ID NO:	8951	9206	9941	9941	691	096	1304	2352	2642	2971	2971	3124		3488	3722	3962	4394	4544	4828		4870	4970	5487	5551	5654	5715	2280	6045

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	. Top Hit Descriptor
6148	16021	26161	1.41	3.4E-01	AI468082.1	EST_HUMAN	tm63g05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
6943	16821		1.77	3.4E-01	AA337063.1	EST_HUMAN	EST41765 Endometrial tumor Homo sapiens cDNA 5' end
7139	17016	27209	1.62	3.4E-01	9633624	NT	Bovine enterovirus strain K2577, complete genome
7313	17189		3.88	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
7313	17189	27391	3.88	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
7433	16446	26635	4.17	3.4E-01	U19492.1	Z	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7433	16446	26636	4.17	3.4E-01	U19492.1	TN	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7690	17540	27766	2.22	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
8380	18257		4.09	3.4E-01	AE000881.1	LN	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
8407		28536	2.2			SWISSPROT	PROBABLE E4 PROTEIN
8440	18314	28572	2.26	3.4E-01	AF045981.1	IN	Rutilus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
8604	18471	28742	1.77	3.4E-01	M25856.1	N	Human von Willebrand factor gene, exons 36 and 37
8604		28743	1.77	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
8790	18605	28895	1.8	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-gicerin/MUC18, complete cds
8814	18627	28916	4.03	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9020	18814		2.01	3.4E-01	U93604.1	NT	Ottrus variegation virus putative replicase gene, partial cds
9130	18887		1.3	3.4E-01	Z21621.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
9229	19508		1.82	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Owf8p (cwf8) gene, complete cds
9347	19024		4.9	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds
							hy42h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.t3
9378	- 1		2.49	3.4E-01	BE218652.1	ESI_HUMAN	PIKO repetitive element;
9432			2.13	3.4E-01	9838361 NT	LN.	Beta vulgaris mitochondrion, complete genome
9537	19140	25264	1.79	3.4E-01	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B
9829	19330		1.79	3.4E-01	AF019413.1	NT	(Bf), and complement component C2 (C2) genes,>
14	10000		7.91	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5JI nodX gene
100	10000	19791	3.92	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5JI nodX gene
440	10384	20208	1.16	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
617			1.41		7662485	N	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1182	11093	20940	3.05	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17

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					2		
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1285	11193		4.82	3.3E-01	BF568880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE;4300251 3'
1588	11492	21352	1.11	3.3E-01	_	INT	Mus musculus disintegrin 5 (Dtgn5), mRNA
1704			1.05		AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week I Homo sapiens cDNA 5' end
2355	12235		4.74		4507834 NT	뉟	Homo sepiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5- decarboxylase) (UMPS) mRNA
2919		22648	7	3.3E-01	AJ251805.1	TN	Bacteriophage phi-YeO3-12 complete genome
2982			1.12		002743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3016	12944	22737	1.01	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus mithramycin biosynthetic genes
3450	13367	23173	1.14		AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3738	13650	23433	2.17	3.3E-01	084645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3884	13795	23582	1.59	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3920	13829		1.92	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4271	14170		2.74		D31662.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
	١.					1471	tp78b12.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN
4589			1.48		AI539114.1	ESI_HUMAN	PET IDE IKANSTOKIEK I (HOMAN)
5263	15185	24960	2.68	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5263	15185		2.68	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5622	1	25623	2.71	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
5622	l		2.71	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6117	16011	26148	3.64	3.3E-01	AI628131.1	EST HUMAN	ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element;contains element L1 repetitive element ;
	Ι				_		ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu
6117	16011	26149	3.64	3.3E-01	AI628131.1	EST HUMAN	repetitive element, contains element L1 repetitive element;
6575	16433	26616	1.5	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
6981	16858		19.46	3.3E-01	BF683954.1	EST_HUMAN	602/40372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
7477	_				N69866.1	EST_HUMAN	za67h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297649 3'
7507	L				BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
7739			2.07	3.3E-01	L41044.1	LN	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
8104					X63953.1	L	D.mauritiana Adh gene
8104	17994	28243			X63953.1	LN	D.mauritiana Adh gene
8389	18265		1.82			EST_HUMAN	602070802F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213585 5'
8561	18431	28700	12.76	3.3E-01	BE219351.1	EST_HUMAN	hv51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 31